

19-65507

CC
DR
EMBL; M01194; AAA4477.1; ALT_FRAME.
DR
DR
PIR; A42784; A42784.
DR
SGD; S001924.
DR
InterPro; IPR00340; DS_phosphatase.
DR
InterPro; IPR00307; TYR_phosphatase.
DR
InterPro; PR00037; DS_P; 1.
DR
SMART; SM00195; DPC; 1.
DR
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW
Cell cycle: Hydrolase.
FT ACT_SITE 283 283 BY SIMILARITY.
SEQUENCE 551 AA; 61906 MW; 4EB3985DFA3FD823 CRC64;
Query Match 17.2%; Score 137.5; DB 1; Length 551;
Best Local Similarity 28.0%; Pred. No. 2.9e-06;
Matches 30; Conservative 20; Mismatches 34; Indels 23; Gaps 3;
QY 27 HMQFLLDIGVRHIVSLTERGPPHSIDSCPGLTMLRLRIPDFCPPADQIDRFVQIVDEANA 86
Db 238 HFE---DGIQHDLIEDG----TCRDLSI-----VKNFVGAETIK 274
QY 87 RGAIVGVHALGSGRTGMLACIYKVERGLAAGDAIAEIRRRLRPGSI 133
Db 275 RGKKAIVHKAGIAGRGLIGALIYTGYFTANECLGICFLRFIRPGMV 321
RESULT 2
PPIP3_DICDDI STANDARD; PRT; 989 AA.
ID PPIP3_DICDDI
AC P54637;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Protein-tyrosine Phosphatase 3 (EC 3.1.3.48) (Protein-tyrosine-
phosphate phosphotyrolidase 3).
GN (PPIP3 OR PIP3) AND (PPIP2 OR PIP3).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX;
RX MEDLINE=96189126; PubMed=8668311; Firtel R.A.;
RA Gamper M., Howard P.K., Hunter T., Firtel R.A.:
RT "Multiple roles of the novel protein tyrosine phosphatase PTP3 during
Dictyostelium growth and development.";
RL Cell Biol. 16:2431-2444(1996);
CC -1- FUNCTION: SEEMS TO DEPHOSPHORYLATE A PROTEIN OF 130 kDa (P130).
-1- CATALYTIC ACTIVITY: Protein tyrosine Phosphate + H(2)O = protein
tyrosine + phosphate.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- TISSUE SPECIFICITY: IN THE ANTERIOR-LIKE AND PRESTALK CELL TYPES.
-1- DEVELOPMENTAL STAGE: EXPRESSED AT MODERATE LEVELS DURING GROWTH
AND DEVELOPMENT.
-1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC
EMBL; U38197; ARG47041.1; -.
DR HSSP; Q06124; 2SP.
DR DDC0111; ptpp1.
DR Dictpb; DD07777; ptpp2.
DR InterPro; IPR00387; TYR_phosphatase.
DR InterPro; IPR00242; Tyr_PP.
DR
DR pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PRO0700; PTYRPhPTase.
DR SMART; SM00194; PTIC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
FT ACT_SITE 649 649 BY SIMILARITY.
FT DOMAIN 460 716 PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN 64 71 POLY-ASN.
FT DOMAIN 109 118 POLY-TASN.
FT DOMAIN 137 190 POLY-ASN.
FT DOMAIN 249 257 POLY-SER.
FT DOMAIN 258 265 POLY-THR.
FT DOMAIN 286 289 POLY-ASN.
FT DOMAIN 366 371 POLY-SER.
FT DOMAIN 834 839 POLY-GLN.
FT DOMAIN 883 892 POLY-GLN.
FT DOMAIN 906 914 POLY-ASN.
FT DOMAIN 943 963 POLY-ASN.
SEQUENCE 989 AA; 10995 MW; 9371105AF80974AF CRC64;
Query Match 15.0%; Score 119.5; DB 1; Length 989;
Best Local Similarity 28.0%; Pred. No. 0.00036; 48; Indels 25; Gaps 5;
Matches 37; Conservative 22; Mismatches 48; Indels 25; Gaps 5;
QY 33 DLGVR-HIVSLTERGPPHSIDSCPGLTMLRLRIPDF-CPPAPQDIDRFVQIVDEANRGE 89
Db 583 DIGVSSLHIIKKGSEFPREV---VLHLYTQWPDCCGAPPSSSHIRTLSVMMNTFKARG 637
QY 90 A-----VGVHCALGFGRGTGMLACYL-----VKEVLAAGDAIAEIRRRLRPGSI 132
Db 638 AKNNNGPVIVHCSCAGIGSGTFISININNAKIERFGNDPSQMNISIKDSVLELRQRGM 697
QY 133 LEYQEQAQFQ 144
Db 698 VOTLDQYIFIFK 709
RESULT 3
DUSB_MOUSE STANDARD; PRT; 663 AA.
ID DUSB_MOUSE
AC 00112;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE Dual specificity protein phosphatase 8 (EC 3.1.3.48) (EC 3.1.3.16)
DE (National Tyrosine Threonine Phosphatase 1).
GN DUSB OR NTPP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=brain;
RX MEDLINE=96311565; PubMed=8733137;
RA Theodouli A.M., Rodrigues N.R., Nesbit M.A., Ambrose H.J.,
RA Paterson H., McLellan-Arnold E., Boyd Y., Leversha M.A., Owen N.,
RA Blake D.J., Ashworth A., Davies K.E.;
RT A member of the MAP kinase phosphatase gene family in mouse
containing a complex triucleotide repeat in the coding region.";
RL Hum. Mol. Genet. 5:675-684 (1996).
CC -1- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.

CC -I SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.

CC -I SIMILARITY: CONTAINS 1 RHODANSE DOMAIN.

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CC

DR EMBL: X95518; CAA64772.1; -.

DR HSSP; Q16828; IMPL.

DR MGI; MG1:06626; Ntpp1.

DR InterrPro: IPR003140; DS_phosphatase.

DR InterPro: IPR01765; Rhodanese like.

DR InterPro: IPR003187; TYR_Phosphatase.

DR Pfam: PF00782; DSPC; 1.

DR SMART; SM0015; DSPC; 1.

DR SMD0450; RHOD; 1.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

DR PROSITE; PS50505; TYR_PHOSPHATASE_2; 1.

DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.

KW Hydrolase; Nuclear protein.

FT DOMAIN 13 136 RHODANSE.

FT DOMAIN 162 432 PROTEIN-TYROSINE PHOSPHATASE.

FT DOMAIN 452 459 POLY-ARG.

FT DOMAIN 555 558 POLY-SER.

FT DOMAIN 559 576 POLY-GLYX.

FT DOMAIN 577 600 POLY-SER.

FT DOMAIN 311 552 PRO-RICH.

FT ACT_SITE 246 246 BY SIMILARITY.

SQ SEQUENCE 663 AA; 68847 MW; 416F429A12C1EA7C CRC64;

Query Match . 14.5%; Score 115.5; DB 1; Length 663; Best Local Similarity 24.1%; Pred. No. 0.00059; Matches 41; Conservative 26; Mismatches 64; Indels 39; Gaps 6;

Qy 8 FSWVLLPGRLAG-----LALPRLPA-----HYOFFLDGLYRHVLSTERGP 48

Db 129 PSCCFPGCLCEKRPATLPSMSISQPCLEPVPSVGLTRILPHLYLGSQDVNLNDLWTGNGIS 188

Qy 49 H----SDSCPG----LTHRLRIP--DFCPAPPDDIDRFVQIVDEBANRGAEVGVHCA 97

Db 189 YVLNASNNSCPKPDFICESRFMRIPINDNYCYKLPWLDSKFIDRAKLSCQVTHCLA 248

Qy 98 GFGRTGTMAGLIVKVERGLAAGDAEIRRURP-----GSIETYEQ 138

Db 249 GISRSATIAIAYIMKTMGMSSDAYRFVKDRRPSISPNFNFGLQLEYER 298

RESULT 4

MCE1_HUMAN STANDARD; PRT; 597 AA.

ID MCE1_HUMAN STANDARD; PRT; 597 AA.

AC 06942; O43483; 060351; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE mRNA capping enzyme (HCE) (HCAP1) [Includes: Polynucleotide 5'-triphosphatase (EC 3.1.3.33) (mRNA 5'-triphosphatase) (TPase); mRNA guanylyltransferase (GTase)]. RNR7 OR CAP1A.

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Gnathostomata; Amniota; Eutheria; Placentalia; Mammalia; Buteraria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_Taxid=9606; [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RP MEDLINE=98058741; PubMed=9371772;

RA Yue Z., Maldonado E., Pillutla R., Cho H., Reinberg D., Shatkin A.J.;

RA *Mammalian capping enzyme complements mutant Saccharomyces cerevisiae

RP lacking mRNA guanylyltransferase and selectively binds the elongating form of RNA polymerase II;".

RT Form of RNA polymerase II;".

RT Proc. Natl. Acad. Sci. U.S.A. 94:12898-12903 (1997).

RT [2]

RT SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3), AND MUTAGENESIS.

RT MEDLINE=98181073; PubMed=9512541;

RA Yamada-Okabe T., Doi R., Shimmi O., Arisawa M., Yamada-Okabe H.; Isolation and characterization of a human cDNA for mRNA 5'-capping enzyme;".

RT Nucleic Acids Res. 26:1700-1706(1998).

RT [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 4).

RC TISSUE-Colon adenocarcinoma;

RX MEDLINE=98139874; PubMed=473487;

RA Tsukamoto T., Shibusaki Y., Murakoshi T., Suzuki M., Nakamura A., Gotoh H., Mizumoto K..

RT Cloning and characterization of two human cDNAs encoding the mRNA capping enzyme;".

RL Biochem. Biophys. Res. Commun. 243:101-108(1998).

CC FUNCTION: BI-FUNCTIONAL mRNA CAPPING ENZYME EXHIBITING RNA 5'-TRIPHOSPHATASE ACTIVITY IN THE N-TERMINAL PART AND mRNA GLANYLYLTRANSFERASE ACTIVITY IN THE C-TERMINAL PART. CATALYZES THE FIRST TWO STEPS OF CAP FORMATION: BY REMOVING THE GAMMA-PHOSPHATE FROM THE 5'-TRIPOPHATE END OF NASCENT MENA TO YIELD A DIPHOSPHATE END, AND BY TRANSFERRING THE GMP MOIETY OF GTP TO THE 5'-DIPHOSPHATE TERMINUS.

CC -I CATALYTIC ACTIVITY: 5'-phosphopolynucleotide + H(2)O = polynucleotide + phosphate.

CC -I CATALYTIC ACTIVITY: GTP + (5')PP-pur-mRNA = diphosphate + G(5')PP-pur-mRNA.

CC -I SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -I ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; 1/MCE1/MCAP1 (SHOWN HERE); 2/HCE1A; 3/HCE1B; 4/HCAP1; ARE PRODUCED BY ALTERNATIVE SPlicing.

CC -I TISSUE SPECIFICITY: ISOFORMS 1 AND 4 (AT A LESSER EXTENT) ARE EXPRESSED IN CEREBRUM, CEREBELLUM, THYROID, LUNG, HEART, LIVER, KIDNEY, SPLEEN, LARGE INTESTINE, TESTIS, SKIN AND MUSCLE.

CC -I MISCELLANEOUS: ISOFORMS 2 TO 4 LACK MENA 5'-GUANYLYLTRANSFERASE ACTIVITY DUE TO DISRUPTIONS OF THE GTPase DOMAIN.

CC -I SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY.

CC -I SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO THE EUKARYOTIC GTPase family.

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CC

DR EMBL; AF025654; ARB9159.1; -.

DR EMBL; AB003022; BAA2894.1; -.

DR EMBL; AB003023; BAA25895.1; -.

DR EMBL; AB003024; BAA2896.1; -.

DR EMBL; AB012142; BAA23198.1; -.

DR EMBL; AB012143; BAA23199.1; -.

DR Genew; HGNC:10073; RNCTT.

DR MM: 603512; -.

DR InterPro: IPR003340; DS_phosphatase.

DR InterPro: IPR003387; TYR_phosphatase.

DR InterPro: IPR00339; mRNA_cap_enzyme.

DR Pfam: PF01331; mRNA_cap_enzyme; 1.

DR SMART; SM0012; PTPC_DSPC; 1.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

DR mRNA_processing; mRNA_capping; Transferase; Nucleotidyltransferase; KW Hydrolase; Multifunctional enzyme; Alternative splicing; KW Nuclear protein.

FT DOMAIN 212 TPE.

FT DOMAIN 229 597 GRASE.

FT DOMAIN 195 205 ASP/GLU-RICH.

FT	ACT-SITE	126	126	RNA 5'-TRIPHOSPHATASE (BY SIMILARITY).
FT	ACT-SITE	294	294	GUANYLYLATION SITE.
FT	VANSPLC	446	446	MISSING (IN ISOFORM 2 AND ISOFORM 3).
FT	VARSPLIC	481	597	MISSING (IN ISOFORM 3).
FT	VARSPLIC	504	597	TKEIQLQDNKTECPEPFENDTAAQGOKRHHDPNTAM VCNSKPKVREKPEPPFENPDKSFPNAYNTAMA PPPPKKRPPLT -> CLEFSVILLEDVLISGIRHNLANN QHHSQSISLLG (IN ISOFORM 4).
FT	MUTAGEN	294	294	K->A: LOSS OF GTASE ACTIVITY.
FT	MUTAGEN	299	299	R->K: LOSS OF GTASE ACTIVITY.
FT	MUTAGEN	345	345	E->K: LOSS OF GTASE ACTIVITY.
FT	MUTAGEN	458	458	K->A: LOSS OF GTASE ACTIVITY.
FT	MUTAGEN	460	460	K->A: LOSS OF GTASE ACTIVITY.
FT	CONFLICT	30	30	M -> I (IN REF. 1).
FT	CONFLICT	484	484	P (IN REF. 1).
FT	SEQUENCE	597 AA;	60556 MW;	51CEECIB190603DE CRC64;
Query Match		14 4%	Score 115:	DB 1; Length 597;
Best Local Similarity		30.0%	Pred. No. 0.00058;	
Matches	24;	Conservative	18;	Mismatches 36; Indels 2; Gaps 1;
Qy	69	PAPQDIDRQVQIDEANARG - EAVGWHICALGIGRTGIGMLACIVLKVERGLAAGDAIEIR	126	
Db	98	PPTTENTETTTRICLGERFERNRNPPELIGVHGTHGFRGELCAFLVEKMDNSIERAVATTA	157	
Qy	127	RLRPSGSIYEQKAVFERY	146	
Db	158	QARPPGIGKKGDYLKFRRY	177	
RESULT 5				
MEBL_MOUSE	STANDARD:	PRT:	597 AA.	
AC	055236;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	mRNA capping enzyme (HCE1) [Includes: Polynucleotide 5'-triphosphatase] (TPase); mRNA triphosphatase (EC 3.1.3.33) (mRNA 5'-triphosphatase) (TPase); mRNA guanylyltransferase (EC 2.7.7.50) (GTP--RNA guanylyltransferase) (Grase).			
GN	RNCT OR CAPA.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-294.			
RX	MEDLINE=98058741; PubMed=931772;			
RA	Yue Z., Maldonado E., Pilutti R., Cho H., Reinberg D., Shatkin A.J.; RT			"Mammalian capping enzyme complements mutant Saccharomyces lacking mRNA guanylyltransferase and selectively binds the elongating form of RNA polymerase II.";
RT	Proc. Natl. Acad. Sci. U.S.A. 94:12898-12903(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98070332; PubMed=9407024;			
RA	McCracken S., Fong N., Rosonina E., Yankulov K., Brothers G., Siderovski D., Hessel A., Foster S., Shuman S., Bentley D.L.; RT			"5'-Capping enzymes are targeted to pre-mRNA by binding to the phosphorylated carboxy-terminal domain of RNA polymerase II.";
RT	Genes Dev. 11:3306-3318(1997).			
RN	[3]			
RP	CHARACTERIZATION, AND MUTAGENESIS.			
RX	MEDLINE=9845533; PubMed=9770468;			
RA	Wen Y., Yue Z., Shatkin A.J.; RT			"Mammalian capping enzyme binds RNA and uses protein tyrosine phosphatase mechanism.";
RL	Proc. Natl. Acad. Sci. U.S.A. 95:12226-12231(1998).			
CC	- FUNCTION: BIFUNCTIONAL mRNA CAPPING ENZYME EXHIBITING RNA 5'-TRIPHOSPHATASE ACTIVITY IN THE N-TERMINAL PART AND mRNA GUANYLYLTRANSFERASE ACTIVITY IN THE C-TERMINAL PART. CATALYZES THE FIRST TWO STEPS OF CAP FORMATION: BY REMOVING THE GAMMA-PHOSPHATE			
CC				
CC	FROM THE 5'-TRIPHOSPHATE END OF NASCENT mRNA TO YIELD A DIPHOSPHATE END, AND BY TRANSFERRING THE GMP MOIETY OF GRP TO THE 5'-DIPHOSPHATE TERMINUS.			
CC	- CATALYTIC ACTIVITY: 5'-Phosphopolynucleotide + H(2)O = Polynucleotide + Phosphate.			
CC	- CATALYTIC ACTIVITY: GTP + (5')PP-pur-mRNA = diphosphate + G(5')PPP-pur-mRNA.			
CC	- ENZYME REGULATION: RNA TRIPHOSPHATASE ACTIVITY IS INHIBITED BY VANADATE, TODEACETATE, AND MAGNESIUM.			
CC	- SUBCELLULAR LOCATION: Nuclear.			
CC	- MISCELLANEOUS: Binds to the elongating phosphorylated form of RNA polymerase II can interact indirectly by binding to POF II C-terminal domain and directly by RNA binding. The GTase domain, rather than the TPase domain mediates these interactions.			
CC	RATHER THAN THE TPASE DOMAIN SECTION; BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN TYROSINE PHOSPHATASE FAMILY.			
CC	- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE EUKARYOTIC GTASE FAMILY.			
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CC	DR EMBL; AF035653; AAB81558_1; -.			
CC	DR InterPro; IPR000340; DS_phosphatase.			
CC	DR InterPro; IPR000387; TYR_phosphatase.			
CC	DR Pfam; PF01331; mRNA_cap_enzyme; 1.			
CC	SMART; SM00012; PTPE_DSPC; 1.			
CC	DR PROSITE; PS50056; TYR_PHOSPHATASE_1; 1.			
CC	DR RNA_processing; mRNA_capping; Transf erase; Nucleotidyltransferase; Nucleic acid hydrolase; Multifunctional enzyme; Nuclear protein.			
CC	FT DOMAIN 1 212			
CC	FT DOMAIN 2 212			
CC	FT ACT-SITE 126			
CC	FT ACT-SITE 294			
CC	FT MUTAGEN 36			
CC	FT MUTAGEN 66			
CC	FT MUTAGEN 110			
CC	FT MUTAGEN 125			
CC	FT MUTAGEN 126			
CC	FT MUTAGEN 132			
CC	FT MUTAGEN 133			
CC	FT MUTAGEN 138			
CC	FT MUTAGEN 168			
CC	FT MUTAGEN 290			
CC	FT MUTAGEN 294			
CC	FT MUTAGEN 315			
CC	FT MUTAGEN 315			
CC	FT MUTAGEN 530			
CC	FT MUTAGEN 530			
CC	FT MUTAGEN 533			
CC	FT MUTAGEN 533			
CC	K->A: NO EFFECT.			
CC	K->A: LOSS OF GTASE ACTIVITY.			
CC	R->A: ALMOST COMPLETE LOSS OF RNA BINDING			
CC	AND LOSS OF GTASE ACTIVITY.			
CC	R->A: AT LEAST 60% OF RNA BINDING			
CC	ACTIVITY AND LOSS OF GTASE ACTIVITY.			
CC	R->A: ALMOST COMPLETE LOSS OF RNA BINDING			
CC	AND LOSS OF GTASE ACTIVITY.			
CC	R->K: LOSS OF GTASE ACTIVITY.			
CC	K->A: ALMOST COMPLETE LOSS OF RNA BINDING			
CC	AND LOSS OF GTASE ACTIVITY.			
CC	K->R: AT LEAST 60% OF RNA BINDING			
CC	ACTIVITY AND LOSS OF GTASE ACTIVITY.			
CC	N->A: ALMOST COMPLETE LOSS OF RNA BINDING			
CC	AND LOSS OF GTASE ACTIVITY.			
CC	N->Q: AT LEAST 60% OF RNA BINDING			
CC	ACTIVITY AND LOSS OF GTASE ACTIVITY.			

	Query Match	Score 14.4%;	Score 11.5;	DB 1;	Length 597;	BY SIMILARITY.
	Best Local Similarity	30.0%;	Pred. No. 0.00058;			
Matches	24;	Conservative	18;	Mismatches	36;	Indels 2;
Indels	2;	Gaps	1;			
Db	98	PAPDQIDRFVQIVDEANARG-	EAVGVHCAAGFGGRGTMALACYLVKERGLLAGDAATEAIR	126		
Oy	69	PTTENTTFIRLCERFERNERSPEPELIGVHCTHGFNRITGLICFLVERMDNSTEAATFA	157			
Oy	127	RURPGSIEVYQEKAQFQY	146			
Oy	: 1 : ; : ;					
Db	158	QARPPGTYKGKQYKLKEFRRY	177			
RESULT 6						
DUS8_HUMAN	ID	DUS8_HUMAN	STANDARD;	PRT;	625 AA.	
AC	Q13202;					
DT	15-JUL-1999	(Rel. 38, Last sequence update)				
DT	15-JUL-1999	(Rel. 38, Last sequence update)				
DE	Dual specificity protein phosphatase 8 (EC 3.1.3.48) (EC 3.1.3.16)					
GN	DUSP8 OR VH5.					
OS	Homo sapiens (Human).					
OC	Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
OX	NCBI_TAXID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE="fetal brain"; PubMed=7561881;					
RX	MEDLINE=96090533;					
RX	Martinez K.J., Seasholtz A.R., Kwak S.P., Clemens K.K., Dixon J.E.,					
RT	"VH5: a Protein tyrosine phosphatase abundant in brain that					
RT	inactivates mitogen-activated protein kinase.";					
RL	J. Neurochem. 65:1823-1833(1995).					
CC	-I- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY SIMILARITY).					
CC	-I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.					
CC	-I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.					
CC	-I- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, HEART, AND SKELETAL MUSCLE.					
CC	-I- SIMILARITY: BELONGS TO THE NON RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.					
CC	-I- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.					
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CC	EMBL; U27193; AAA83151.1; -.					
DR	HSSP: HGNC:3074; DUSP8.					
DR	MM: 602038; -.					
DR	InterPro; IPR00340; DS_phosphatase.					
DR	InterPro; IPR001763; Rhodanese-like.					
DR	InterPro; IPR000387; TYR_Dphosphatase.					
DR	PFAM; PF00782; DUSP8.					
DR	SMART; SM00195; DUSP8.					
DR	SMART; SM00450; RHOD; 1.					
DR	Prosite; PS0033; TYR_Phosphatase_1.					
DR	Prosite; PS0056; TYR_Phosphatase_2; 1.					
DR	Prosite; PS0054; TIR_Phosphatase_DUAL; 1.					
KW	Hydrolyase; Nuclease; Protein.					
FT	DOMAIN 13 136 RHOANESE.					
FT	DOMAIN 162 430 PROTEIN-TYROSINE PHOSPHATASE.					
FT	DOMAIN 310 550 PRO-RICH.					
RESULT 7						
PPN_NPYAC	ID	PPN_NPYAC	STANDARD;	PRT;	168 AA.	
AC	P24656;					
DT	01-MAR-1992 (Rel. 21, Last sequence update)					
DT	01-NOV-1995 (Rel. 32, Last sequence update)					
DE	Protein-tyrosine phosphatase (EC 3.1.3.48) (BYF).					
GN	PPN.					
OS	Autographa californica nuclear polyhedrosis virus (ACMNPV).					
OC	Viruses; dsDNA viruses, no RNA stage; Baculoviridae;					
OC	Nucleopolyhedrovirus.					
OX	Nucleopolyhedrovirus.					
NCBI_TAXID=46015;						
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	RA	Tilakarathne N., Hardin S.E., Weaver R.F.;				
RT	CC	"Nucleotide sequence and transcript mapping of the HindIII F region of the Autographa californica nuclear polyhedrosis virus genome.";				
RL	J. Gen. Virol. 72:285-291(1991).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-C6,					
RX	RA	MEDLINE=92024079; PubMed=1926775;				
RT	RA	Possee R.D., Sun T.P., Howard S.C., Ayres M.D., Hill-Perkins M., Gearing K.L.; sequence of the Autographa californica nuclear polyhedrosis 9.4 kbp EcoRI-1 and -R (polyhedrin gene) region. ";				
RT	RA	RT	Virolgy 185:229-241(1991).			
RN	[3]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-C6,					
RX	RA	MEDLINE=94303173; PubMed=8030224;				
RT	RA	Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D., "The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.";				
RT	RA	RT	Virology 202:586-605(1994).			
RN	[4]					
RP	CHARACTERIZATION.					
RX	RA	MEDLINE=93186773; PubMed=8444848;				
RT	RA	Sheng Z., Charbonneau H.; "The baculovirus Autographa californica encodes a protein tyrosine phosphatase.";				
RT	RA	J. Biol. Chem. 268:4728-4733(1993).				
CC	-I- FUNCTION: AUTO_DEPHOSPHORYLATES SERYL AND THREONYL RESIDUES.					
CC	-I- CATALYTIC ACTIVITY: Protein tyrosine Phosphate + H(2)O = Protein tyrosine + phosphate.					
CC	-I- MISCELLANEOUS: PROBABLY EXPRESSED LATE IN INFECTION.					
CC	-I- SIMILARITY: BELONGS TO THE NON RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. C001 SUBFAMILY.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.;					

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3] CHARACTERIZATION, AND MUTAGENESIS OF CYS-124.
 RX MEDLINE-97344078; PubMed=900605;
 RA Takagi T.; Moore C.R.; Diehn F.; Buratowski S.;
 RT "An RNA triphosphatase related to the protein tyrosine
 phosphatases";
 RL Cell 89:867-873(1997).
 CC -I- FUNCTION: BIFUNCTIONAL mRNA CAPPING ENZYME EXHIBITING RNA 5'-
 TRIPHOSPHATASE ACTIVITY IN THE N-TERMINAL PART AND mRNA
 GUANYLYLTRANSFERASE ACTIVITY IN THE C-TERMINAL PART. CATALYZES THE
 FIRST TWO STEPS OF CAP FORMATION: BY REMOVING THE GAMMA-PHOSPHATE
 FROM THE 5'-TRIPHOSPHATE END OF NASCENT mRNA TO YIELD A
 DIPHOSPHATE END, AND BY TRANSFERRING THE GMP MOIETY OF GTP TO THE
 5'-DIPHOSPHATE TERMINUS.
 CC -I- CATALYTIC ACTIVITY: 5'-phosphopolyribonucleotide + H(2)O =
 CC POLynucleotide + phosphate.
 CC -I- CATALYTIC ACTIVITY: GTP + (5')PP-pur-mRNA = diphosphate +
 CC G(5')PPP-pur-mRNA.
 CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -I- INDUCTION: INHIBITED BY MAGNESIUM.
 CC -I- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE NON-RECEPTOR
 CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY.
 CC -I- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE EUKARYOTIC
 GTASE FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL; AF03925; AB16144.1; -
 DR EMBL; 275525; CAH9765.1; ALT_INIT.
 DR WormPep; C03D6.3; CEL5758.
 DR InterPro; IPR003140; DS_phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR001339; mRNA_cap_enzyme.
 PRFM; PF01331; mRNA_cap_enzyme; 1.
 DR SMART; SM00112; PPIC_DSPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
 KW mRNA_processing; mRNA_capping; transferase; Nucleotidyltransferase;
 KW Hydrolyase; Multifunctional enzyme; Nuclear protein.
 FT DOMAIN 1 212
 FT DOMAIN 229 573
 FT ACT_SITE 124 124
 FT ACT_SITE 299 299
 FT MUTAGEN 124 124
 FT MUTAGEN 124 124
 SQ SEQUENCE 573 AA; 66336 MW; F50AC59F1815F47 CRC64;

Query Match 14.2%; Score 113; DB 1; Length 573;
 Best Local Similarity 36.0%; Pred. No. 0.0088;
 Matches 31; Conservative 12; Mismatches 37; Indels 6; Gaps 3;

Qy 69 PRPDQIDRFVQIVDEANAR--GEAVGVHCAAGFGRTGTMACYL--VKERLIAAGDAIE 124
 Db 96 P^NQEDIDNFNFIKVQEOFHKYKPYDRVGVHCTGFNRIGFLIAAFLQVEEYGLDA-AIGE 153
 Qy 125 IIRLRQSIETYEQEKAQVFOYQRTK 150
 Db 154 FAENRQKGIVKDYIDDLFARDPTE 179

RESULT 10
 DUSC_HUMAN STANDARD; PRT; 340 AA.
 ID DUSC_HUMAN STANDARD; PRT; 340 AA.
 AC 0QUNI6; DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dual specificity Protein phosphatase 12 (EC 3.1.3.48) (EC 3.1.3.16)
 RP (Dual-specificity tyrosine phosphatase YWH1).
 RX DUSP12.
 RA Homo sapiens (Human).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
 OC NCBI_TaxID=9606;
 RN [1]
 RX SEQUENCE FROM N.A., AND CHARACTERIZATION.
 CC "Identification of the human YWH protein-tyrosine phosphatase
 orthologue reveals a novel zinc binding domain essential for in vivo
 function.";
 RT J. Biol. Chem. 274:23991-23995(1999).
 CC -I- CATALYTIC ACTIVITY: Protein tyrosine Phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -I- SUBCELLULAR LOCATION: Nuclear.
 CC -I- TISSUE SPECIFICITY: Ubiquitous, highest expression in spleen,
 CC testis, ovary, and peripheral blood leukocytes and lower
 CC expression in liver and lung.
 CC -I- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY DUAL SPECIFICITY SUBFAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL; AF19226; ARD51134.1; -
 DR EMBL; 016828; IMPR.
 DR Genew; HGNC:3067; DUSP12.
 DR MIN; 604835; -
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000822; Znf_C2H2.
 DR InterPro; IPR000822; Znf_C2H2.
 DR InterPro; IPR000822; Znf_C2H2.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS00093; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; UNKNOWN_1.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; UNKNOWN_1.
 FT Hydrolease; Zinc; Metal-binding.
 DOMAIN 88 160
 FT ACT_SITE 115 115
 SQ SEQUENCE 340 AA; 37687 MW; 56B52192B42C73EB CRC64;

Query Match 14.0%; Score 111.5; DB 1; Length 340;
 Best Local Similarity 28.4%; Pred. No. 0.0069;
 Matches 40; Conservative 26; Mismatches 64; Indels 11; Gaps 6;

Qy 11 VLPG-RLLAGLAIPLRPLAHQFLIDGVRLVLSLTERGPPHSDFSCPGI-TLHLRLIDFCP 68
 Db 30 VQPG-LRLAGLAIPLRPLAHQFLIDGVRLVLSLTERGPPHSDFSCPGI-TLHLRLIDFCP 85
 Qy 69 PAPD--QIDREVQIVDEANARGEAVGVHCAAGFGRTGTMACYLKVERGLAAGDAIE 125
 Db 86 PETDLISHLDRCAVFTGQQAEGRAVLYVCHAGVSRSVAlITAFLMTDQLPFKEAYKL 145
 Qy 126 RLRPQS--IEVYEQEKAVQ 144
 Db 146 QIKPEAKMNCFEWQKLYQ 166

RESULT 11
 PPT1_NPWP

ID PTP1_NPVP0 - STANDARD; PRT; 220 AA.
 AC 010274;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative protein-tyrosine phosphatase 1 (EC 3.1.3.48).
 GN PTP-1.
 OS Orgyia pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedroviruses.
 OX NCBI_TaxID=164623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97271300; PubMed=9126251;
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 RA Rohmann G.F.;
 RT "The sequence of the *Orygia pseudotsugata* multinucleocapsid nuclear
 polyhedrosis virus genome.";
 RL Virology 229:381-399(1997).
 CC -!- FUNCTION: COULD BE INACTIVE AS THE ACTIVE SITE CYSTEINE IS
 MODIFIED TO TRITYPTOPHAN.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 TYROSINE PHOSPHATASE FAMILY. CDC14 SUBFAMILY.
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 CC EMBL; U05930; AAC39009; 1; -;
 CC InterPro; IPR00340; DS_phosphatase.
 DR SMART; SM00012; PTMc_DSPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 KW Hydrolase.
 FT SITE 162 162 EQUIVALENT OF ACTIVE SITE CYS.
 SQ SEQUENCE 220 AA; 25234 MW; D3FC09391953D425 CRC64;
 Query Match 13 4%; Score 107; DB 1; Length 220;
 Best Local Similarity 32.9%; Pred. No. 0.0012;
 Matches 27; Conservative 13; Mismatches 40; Indels 2; Gaps 1;
 QY 55 GLIYHLRLRPDPFPAPPOIDRIVQIVDEANAREA - VGVHKAIGRSGPTGMLACYLVR 112
 Db 120 GLYKKKIRPYGRAVPDIDVAFETVDFEFFRCPMTMLVAVHWTGLNRSGYLVCRYAVE 179
 QY 113 ERGLAAGDATAETRRLPGSIE 134
 Db 180 RIYVSPTDAIRRFSTARGHIE 201
 RESULT 12
 DUS9_HUMAN STANDARD; PRT; 384 AA.
 ID DUS9_HUMAN STANDARD; PRT; 384 AA.
 AC 099956;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dual specificity protein phosphatase 9 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Mitogen-activated protein kinase phosphatase 4) (MAP kinase
 phosphatase 4) (MAP-4).
 DE DUSP9 OR MKP4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97184169; PubMed=9030581;
 RA Muda M., Boschart U., Smith A., Antonsson B., Gillieron C.,
 RA Chabert C., Camps M., Martinou J., Ashworth A., Arkinstall S.;
 RT "Molecular cloning and functional characterization of a novel
 mitogen-activated protein kinase phosphatase, MKP-4.";
 RL J. Biol. Chem. 272:5141-5151(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Platzer M.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INACTIVATES MAP KINASES. HAS A SPECIFICITY FOR THE ERK
 FAMILY.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 tyrosine + phosphate.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 TYROSINE PHOSPHATASE FAMILY DUAL SPECIFICITY SURFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; U05111; AAF74507; 1;
 DR HSSP; Q16828; IMKP.
 DR Genew; HGNC:3076; DUSP9.
 DR MIM; 300134; -;
 DR InterPro; IPR00340; DS_Phosphatase.
 DR InterPro; IPR01763; Rhodanese-like.
 DR InterPro; IPR00387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR SMART; SM00195; DSPC; 1.
 DR SMART; SM00450; RHOD; 1.
 DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_DUAL; 1.
 DR PROSITE; PS00583; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS50054; TYR_PHOSPHATASE.
 KW Hydrolase.
 FT DOMAIN 8 137 RHODANESE.
 DOMAIN 203 384 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 290 290 BY SIMILARITY.
 SQ SEQUENCE 384 AA; 41867 MW; F559BCA95AB379B7 CRC64;
 Query Match 13 4%; Score 107; DB 1; Length 384;
 Best Local Similarity 25.5%; Pred. No. 0.0022;
 Matches 36; Conservative 25; Mismatches 56; Indels 24; Gaps 4;
 QY 2 GVQQPNFS-----WVLPGRLAGLALPRLPAHYQFLDLGVRLVSLTERGPSPHSSCP 54
 Db 191 GATPPPGVGLRASFPVQILNLNYLGSAA-R-FDSANLESLAKLGIRYILNYPNLPFFERNG 248
 QY 55 GLIYHLRLRPD-----FCPPAPDQTDRFVQIVDEANARGAVGVICALGFTGTML 106
 Db 249 DEHYKOIPISDHMSQLNSRFFPEA-----IEFIDEALSQNCGVLYVHCLAGVSRVWT 301
 QY 107 ACYLVKVERGLAAGDAETRRL 127
 Db 302 VAYLMQKHLISLNDYDIKKR 322
 RESULT 13
 PTP3_CHIEU STANDARD; PRT; 276 AA.
 ID PTP3_CHIEU
 AC Q39491;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE dual specificity protein phosphatase (EC 3.1.3.48) (EC 3.1.3.16).
 GN VH-PTP13.
 OS Chlamydomonas eugametos.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3053;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=UTEX 10;
 RX MEDLINE=95321001; PubMed=7599654;
 RA Haring M.A., Siderius M., Jonak C., Hirt H., Walton K.M.,
 RA Musgrave A.;
 RT "Tyrosine phosphatase signalling in a lower plant: cell-cycle and
 RT oxidative stress-regulated expression of the Chlamydomonas eugametos
 RT VH-PTP13 gene.";
 RL plant J. 7:981-988(1995).
 CC -1- FUNCTION: COULD BE INVOLVED IN TYROSINE PHOSPHATASE SIGNALLING
 CC PATHWAYS: HAVING MAP-KINASES AS SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H₂O = protein
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -1- DEVELOPMENTAL STAGE: NONDIVIDING GAMETES DID NOT EXPRESS THE VH-
 CC PTP13 GENE WHEREAS SYNCHRONOUSLY DIVIDING VEGETATIVE CELLS ONLY
 EXPRESSED VH-PTP13 IN THE EARLY GI-PHASE OF THE CYCLE.
 CC -1- INDUCTION: BY OXIDATIVE STRESS.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X77938; CAM54910.1; -.
 DR HSSP; P51422; IYVR.
 DR InterPro; IPR000340; DS_phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR pfam; PF00782; DSPC; 1.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolase.
 FT DOMAIN 89 276 CATALYTIC.
 FT ACT_SITE 172 172 C->S: INACTIVE.
 FT MUTAGEN 172 172 C->S: INACTIVE.
 SQ SEQUENCE 276 AA; 30310 MW; 034EB63951E03381 CRC64;
 SQ
 Query Match 13.0%; Score 104; DB 1; Length 276;
 Matches 35; Conservative 21; Mismatches 57; Indels 14; Gaps 4;

Qy 9 SWNLPGRLAGLALPRLPRAHYOFFLDLGVRHVISLER-GPPHSID----SCPGITLHLRL 62
 Db 88 SVIVPGKLI-LSCSVEESESSLTLKGVLVTHIQLQGELKPKSPHGRTYLSFLDMEGD 146
 Qy 63 IPDFCPAPDQIDRFLQIVDNEAARGEAVGPHCALGFGRTMCLACLVKVERGLAGDAI 122
 Db 147 IVALAPSC-----FOFLQDQAQSGVCLVLAGISRSASWVIAVLMWQGMPTEAR 199
 Qy 123 AEIRRLR 129
 Db 200 AMVRRAR 205

RESULT 14
 PTN6_HUMAN

ID	PRIM_HUMAN	STANDARD;	PRT;	595 AA.
DT	P23350;			
AC				
DT				
DT	01-DEC-1992 (Rel. 24, Created)			
DT	15-JUN-2002 (Rel. 41, last sequence update)			
DE	Protein-tyrosine phosphatase, non-receptor type 6 (EC 3.1.3.49) (Protein-tyrosine phosphatase, non-receptor type 6 (EC 3.1.3.49)) (Hematopoietic cell protein-tyrosine phosphatase) (SH-PTP1) (Protein-tyrosine phosphatase SH-1).			
DE	PTPN6 OR PTP1C OR HCP.			
OS	Homo sapiens (Human).			
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX				
NCBI_TaxID=9606;				
[1]				
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
RX	MEDLINE=92122209; PubMed=1132748;			
RA	Yi, T., Cleveland, J.L., Ihle, J.N.;			
RT	"Protein tyrosine phosphatase containing SH2 domains: characterization, preferential expression in hematopoietic cells, and localization to human chromosome 12p12-p13.";			
RT	Shen, S.H., Bastien, L., Posner, B.I., Chretien, P.;			
RL	Mol. Cell. Biol. 12:836-846(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).			
RC	TISSUE-Breast;			
RX	MEDLINE=91143305; PubMed=1652101;			
RA	Shen, S.H., Bastien, L., Posner, B.I., Chretien, P.;			
RT	Nature 353:868-868(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
RX	MEDLINE=92141214; PubMed=1736296;			
RA	Plutzky, J., Neel, B.G., Rosenberg, R.D.;			
RT	"Isolation of a src homology 2-containing tyrosine phosphatase.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:1123-1127(1992).			
RN	[5]			
RP	SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).			
RX	MEDLINE=95994454; PubMed=665105;			
RA	Banville, D., Stocco, R., Shen, S.H.;			
RT	"Human protein tyrosine phosphatase 1C (PTPN6) gene structure: alternate promoter usage and exon skipping generate multiple transcripts";			
RT	Malley, T., Gibbs, R.A., Genomics 27:1165-1173(1995).			
RN	[6]			
RP	SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).			
RX	MEDLINE=96103695; PubMed=8723724;			
RA	Ansari-Tari, M.A., Muzyk, D.M., Lu, J.J., Lu, F., Lilley, C.E., Spanos, S.,			
RA	Malley, T., Gibbs, R.A., RT Genomics 27:1165-1173(1995).			
RT	"A gene-rich cluster between the CD4 and triosephosphate isomerase genes at human chromosome 12p13.";			
RT	Genome Res. 6:314-326(1996).			
RN	[7]			
RP	PHOSPHORYLATION.			
RX	MEDLINE=95300784; PubMed=7781604;			
RA	Li, R.Y., Gaits, F., Ragab, A., Ragab-Thomas, J.M.F., Chap, H.,			
RT	"Tyrosine phosphorylation of an SH2-containing protein tyrosine phosphatase is coupled to platelet thrombin receptor via a pertussis toxin-sensitive heterotrimeric G-protein.";			
RT	EMBO J. 14:2519-2526(1995).			
RN	[8]			
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 248-399.			
RX	MEDLINE=98447672; PubMed=9774441;			
RA	Yang, J., Liang, X., Niu, T., Meng, W., Zhao, Z., Zhou, G.W.;			
RT	"Crystal structure of the catalytic domain of protein-tyrosine phosphatase SHP-1.";			
RT	J. Biol. Chem. 273:2819-2820(1998).			
RL	J. Biol. Chem. 273:2819-2820(1998).			
CC	-1- FUNCTION: PLAYS A KEY ROLE IN HEMATOPOIESIS. THIS PTASE ACTIVITY MAY DIRECTLY LINK GROWTH FACTOR RECEPTORS AND OTHER SIGNALING			

R.A. Gibbs R.A.; Comparative sequence analysis of a gene-rich cluster at human chromosome 12p13 and its syntenic region in mouse chromosome 6. ";

R.T. chromosome 12p13 and its syntenic region in mouse chromosome 6. ";

R.L. Genome Res. 8:29-40(1998).

R.N. [5]

R.P. SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SUBUNIT.

R.C. STRAIN=C3H; TISSUE=Adrenal gland;

R.X. MEDLINE=99348302; PubMed=10419485;

R.A. Martin A., Tsui H.W., Shulman M.J., Isenman D., Tsui F.W.;

R.T. "Murine SHP-1 splice variants with altered Src homology 2 (SH2) domains: Implications for the SH2-mediated intramolecular regulation of SHP-1.";

R.R. J. Biol. Chem. 274:21725-21734(1999).

R.I. [6]

R.P. SEQUENCE FROM N.A.

R.A. Strauberg R.; Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.

R.N. [7]

R.P. SEQUENCE OF 54-68: 128-135; 137-151; 242-252; 278-285; 293-308 AND 373-382, AND PHOSPHORYLATION.

R.X. MEDLINE=93054686; PubMed=1185421;

R.A. "Protein tyrosine phosphatase-1C is rapidly phosphorylated in tyrosine in macrophages in response to colony stimulating factor-1.";

R.T. J. Biol. Chem. 267:2347-2450(1992).

R.L. "FUNCTION: PLAYS A KEY ROLE IN HEMATOPOIESIS. THIS PTASE ACTIVITY MAY DIRECTLY LINK GROWTH FACTOR RECEPTORS AND OTHER SIGNALING PROTEINS THROUGH PROTEIN-TYROSINE PHOSPHORYLATION. THE SH2 REGIONS MAY INTERACT WITH OTHER CELLULAR COMPONENTS TO MODULATE ITS OWN PHOSPHATASE ACTIVITY AGAINST INTERACTING SUBSTRATES.

CC -1 CATALYTIC ACTIVITY: Protein tyrosine phosphate + H₂O = protein

CC tyrosine + phosphate.

CC -1 SUBCELLULAR LOCATION: Cytoplasmic.

CC -1 TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN HEMATOPOIETIC CELLS.

CC -1 ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are produced by alternative splicing.

CC -1 PTM: phosphorylated on tyrosine residues.

CC -1 SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. SUBCLASS THAT CONTAINS SH2 DOMAINS.

CC -1 SIMILARITY: CONTAINS 2 SH2 DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>)

CC

DR InterPro; IPR000242; TYR_PP.

DR Pfam; PF00017; SH2; 2.

DR Pfam; PF0102; Y_phosphatase; 1.

DR PRINTS; PR0070; PR1PFHPTASE.

DR PRINTS; PR0001; SH2DOMAIN.

DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.

DR SMART; SM00194; PIFPC; 1.

DR SMART; SM00222; SH2; 2.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

DR PROSITE; PS5056; TYR_PHOSPHATASE_2; 1.

DR PROSITE; PS5055; TYR_PHOSPHATASE_PTP; 1.

DR KW Hydrolase; SH2 domain; Repeat; Phosphorylation; Alternative splicing.

FT DOMAIN 4 100 SH2 1.

FT DOMAIN 110 213 SH2 2.

FT DOMAIN 269 514 PROTEIN-TYROSINE PHOSPHATASE.

FT ACT-SITE 453 453 BY SIMILARITY.

FT VASPPLIC 1 3 MVR -> MSLRG (IN ISOFORM 2).

FT VASPPLIC 1 39 MISSING (IN ISOFORM 3).

FT VASPPLIC 40 44 SLSR -> MLSRG (IN ISOFORM 3).

FT VARIANT 77 99 EYVQDGITQDNGTITHLYP -> VPRPHTRAGGVTAGGQLAD (IN MOTHERTEN (ME)).

FT VARIANT 100 595 MISSING (IN MOTHERTEN (ME)).

FT CONFLICT 240 240 A -> R (IN REF. 1 AND 3).

FT CONFLICT 572 572 K -> Q (IN REF. 1 AND 3).

FT CONFLICT 586 586 E -> D (IN REF. 6).

FT CONFLICT 595 595 MW; CEF17300D032638D2 CRC64;

SQ SEQUENCE 595 AA; 67559 MW;

Query Match Best Local Similarity Score 13.0%; 104; DB 1; Length 595; Matches 39; Conservative 27.5%; Pred 36; Mismatches 7; Indels 50; Gaps 7;

QY 27 HYOFLLDIGVRHLVSLERGRGPNSDSCPGLTUHLRLIPDFCAPPADQIDRFVQIVDEANA 86

Db 411 HYOYL-----SWPDHGVP--SERGGVVL-----SFLDQINQ 438

QY 87 ROBA-----VGHCALGGFRGRTMIALCYLVKE---RGLAAG---DAIAEIRRURPGS 132

Db 439 ROBSLPHAGPITVHCSAGIGRTGTTIWDLMESISTKGLCDIDIQKTIONVRAORSGM 498

QY 133 IEIYEQEK---AVFQTYRKT 150

Db 499 VDQEAQKFKIVVIAQFETETK 520

Search completed: November 4, 2002, 12:47:03
Job time : 27 secs



F84771 hypothetical protein At2g35680 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C;Accession: F84771
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentov, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: F84771
 A;Status: preliminary
 A;Cross-references: GB:AE002093; NID:94263787; PIDN:AD1547.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g35680
 A;Map position: 2
 Query Match 17.9%; Score 142.5; DB 2; Length 383;
 Best Local Similarity 28.8%; Pred. No. 2.5e-06; Cutoff 31; Mismatches 58; Indels 15; Gaps 6;
 Matches 42; Conservative 31; Mismatches 58;
 Qy 10 WLPGRPLGLAERLPLRPAQFLDLGGRHLVLSLTERGPSPHSQDSCPGILHR-----L 61
 Db 122 WFLQFILLG-AVP-FPSVPQLKELGKGVITNE--PTEIATPS-SLIKSYCIDHVI 175
 Qy 62 RIFDFC-PPAPDODIDRFOIVDPEVDEBANRGEAVGSHCALGFGRGTGMACLYLWVERGLAGD 120
 Db 176 AYFDICFAPSMEALCQAVEFHNRASLGGTIVWCKAGRGSNTIVTCYLWQRKRNMPAA 235
 Qy 121 AYFAIRRURRGPSETYEQEKAFFQFY 146
 Db 236 AVSVRSIRPVVLAQAQKAVVEYY 261

RESULT 11

S56283 protein-tyrosine-phosphatase (EC 3.1.3.48) CDC14 - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: cell division control protein cdc14; protein R005; protein YFR028c
 C;Species: *Saccharomyces cerevisiae*
 C;Accession: S56283; A42784; S58416; S59949; S62239; S63033; S69234
 R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, A.; Description: Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces cerevisiae*
 A;Reference number: S56186
 A;Accession: S56283
 A;Molecule type: DNA
 A;Residues: I-551 <MUR>
 A;Cross-references: EMBL:D50617; NID:9836685; PID:d1009908; PID:9836783; MIPS:YFR028c
 R;Wan, J.; Xu, H.; Grunstein, M.
J. Biol. Chem. 267, 11274-11280, 1992
 A;Title: CDC14 of *Saccharomyces cerevisiae*. Cloning, sequence analysis, and transcriptic
 A;Reference number: A42784; MUID:92283835; PMID:1597462
 A;Accession: A42784
 A;Molecule type: DNA
 A;Residues: MPV1,114,'MRTKSQFRNW',124-125,'A',127,'G',131,'LRKKRL',139,'C',141,'PSI'
 A;Cross-references: EMBL:MG1194; NID:9171182; PID:g171183; EMBL:S37205
 A;Note: sequence extracted from NCBI backbone (NCBIN:104751, NCBIPI:104754)
 R;Mai, B.; Lipp, M.
 A;Reference number: S38416
 A;Accession: S38416
 A;Molecule type: DNA
 A;Residues: M,101, AL',104, 'LKD',110, 'RGGDSSASSASGV',118-421 <MAT>
 A;Cross-references: EMBL:X15077; NID:9407517; PID:9407518
 R;Masaki, S.M.S.; Yasuishi, M.Y.M.; Akio, T.E.A.T.
 A;Submitted to the EMBL Data Library, June 1995
 A;Description: dominant mutants alleles of a yeast protein kinase gene CDC15 suppress th
 A;Reference number: S59694
 A;Accession: S59694

RESULT 12

D75309 protein-tyrosine phosphatase-related protein - *Deinococcus radiodurans* (strain R1)
 C;Species: *Deinococcus radiodurans*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C;Accession: D75309
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Smith, H.O.; Ventresca, R.J.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Ventresca, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: D75309
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: I-177 <WHT>
 A;Cross-references: GB:AE002049; GB:AE000513; NID:96459945; PIDN:AAF11705.1; PID:9645
 C;Genetics:
 A;Gene: DR2161
 A;Map position: 1

Query Match 16.7%; Score 133; DB 2; Length 177;
 Best Local Similarity 38.2%; Pred. No. 8.8e-06; Cutoff 34; Mismatches 15; Indels 8; Gaps 3;

Qy 67 CPPAIDID---RFVQIVDE--ANARGEAVGVHCAALGFRGRTGMALCYLVKERGLAG 119
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 90 CPTIVDGSQVPSDHRARFGLLDELTDLALDGKNTVWHCRGGLGAGLTAACLY-QAGKRPD 148

Qy 120 DIAIEIRRLRPGSIEVQEKAVFQFYQR 148
 |||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 149 DIALVALVRKTRRGAIENARQEQTREFAQ 177

RESULT 13

SI9740 hypothetical protein B - Rhodobacter capsulatus
 C;Species: Rhodobacter capsulatus
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 12-Feb-1999
 C;Accession: SI9740
 R;Kelly, D.J.
 Submitted to the EMBL Data Library, February 1992

A;Reference number: SI9739
 A;Accession: S19740

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-376 <HEI>

A;Cross-references: EMBL:XG33974

C;Superfamily: VHL-type dual specificity phosphoprotein phosphatase homology F;63-182/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>

Query Match 15.7% Score 125; DB 2; Length 376;
 Best Local Similarity 30.4%; Pred. No. 0.0001; Mismatches 49; Indels 22; Gaps 3;
 Matches 38; Conservative 16; MisMatches 49; Indels 22; Gaps 3;

Qy 31 LLDLGVRHLVSLTE-----RGPPHSDSCPGLTILHRLIPDFCPAPDQIDR 76
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 55 IADWGAHVHLTVEPQELGMLKVPLDGTQGR----AGMDWHPPLADSYVTPFAEAR 109

Qy 77 FV--QTVDEANARGEAVGVHCAALGFRGRTGMALCYLVKERGLAAGDAETIRRLRGSI 133
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 110 WQAEGRVIRAALRAGADVWVHCKGGLGRAGMIAARLIVELGADPKAVNAVARTARPGAI 169

Qy 134 ETVYEQ 138
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 170 ETPAQ 174

RESULT 14

T41891 phosphotyrosine phosphatase orf1 - *Bombyx mori* nuclear polyhedrosis virus (isolate T3)

C;Species: *Bombyx mori* nuclear polyhedrosis virus, BmSNPV

A;Variety: Isolate T3
 C;date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000

C;Accession: T41891

R;Gomi, S.; Majima, K.; Maeda, S.

J;Gen. Virol. 80, 1333-1337, 1999

A;Title: Sequence analysis of the genome of *Bombyx mori* nucleopolyhedrovirus.

A;Reference number: 222020; MUID:99281911; PMID:10355780

A;Accession: T41891

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-168 <KAN>

A;Cross-references: EMBL:L33180; PIDN: AAC63820.1; PID:93745973

A;Experimental source: isolate T3

A;Genetics:

A;Note: ptp

C;Superfamily: dual specificity phosphoprotein phosphatase DUSP3; VHL-type dual specific

Query Match 14.9% Score 119; DB 2; Length 168;
 Best Local Similarity 32.6%; Pred. No. 0.0002; Mismatches 41; Indels 4; Gaps 2;
 Matches 29; Conservative 15; MisMatches 41; Indels 4; Gaps 2;

Qy 113 ERLAAGDIAEIRRRLRPGSIE--TYEQQ 139
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 137 TIGIAPOEAINREPKARGHKIERONYVQD 165

RESULT 15

AB2246 probable phosphatase VC1070 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: AB2246

R;Heideberg, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: AB2035; MUID:20406833; PMID:10952301

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: GB:AE004188; GB:AE003852; NID:9655530; PIDN:AAF94229.1; GSPDB:GN

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC1070

A;Map position: 1

Query Match 14.7% Score 117; DB 2; Length 165;
 Best Local Similarity 33.3%; Pred. No. 0.00031; Mismatches 43; Indels 20; Gaps 5;
 Matches 39; Conservative 15; MisMatches 43; Indels 20; Gaps 5;

Qy 35 GVRHLVSLTERGPSPHSIDSCPGLTILHRLIPDFCPAPDQIDRFAQVQ----IVDEANAR 87
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 58 GVGELPAVEKA-----GLOWHARPIEDC---APDA---AFQADQHQCSFHQLHQSLR 105

Qy 88 GEAVGVHCAALGFRGRTGMALCYLVKERGLAAGDAAETIRRLRPGSITMYEQKAVEQ 144
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 106 GERVALHCMGGSGRTG-LLAAMHLLERKGWPPLSITOWQALRPGAFTKKEVQVQYHQ 161

Search completed: November 4, 2002, 12:49:51
 Job time : 45 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

November 4, 2002, 12:43:02 ; Search time 82 Seconds

{without alignments} 376.915 Million cell updates/sec

Title:

US-09-619-380-2

Perfect score:

798 1 MGVOPPNFSWVLPGRLAGLA.....GSITYEQEKAVFQFYQRTK 150

Sequence:

09vz7 09vz7

Scoring table:

BLOSUM62

Gapext 0.5

Searched:

671580 seqs, 20047115 residues

Total number of hits satisfying chosen parameters:

671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL21;*

- 1: sp_archaea;*
- 2: sp_bacteria;*
- 3: sp_fungi;*
- 4: sp_human;*
- 5: sp_invertebrate;*
- 6: sp_mammal;*
- 7: sp_mhc;*
- 8: sp_organelle;*
- 9: sp_phage;*
- 10: sp_plant;*
- 11: sp_rabbit;*
- 12: sp_virus;*
- 13: sp_vertebrate;*
- 14: sp_unclassified;*
- 15: sp_rvirus;*
- 16: sp_bacteriap;*
- 17: sp_archeap;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	798	100.0	150 4	09bvj7 homo sapien
2	99.4	150	4	09nx48 homo sapien
3	90.9	144	11	09cw48 mus musculus
4	242.5	30.4	190	5 P91585 cliona intestinalis
5	186.5	23.4	681	5 P81300 caenorhabditis elegans
6	186.5	23.4	709	5 P81299 caenorhabditis elegans
7	186.5	23.4	1063	5 Q05976 caenorhabditis elegans
8	170.5	21.4	447	4 QY6U00 homo sapien
9	169	21.2	147	1 Q8x270 pyrococcus
10	168.5	21.1	459	4 Q43183 homo sapien
11	168.5	21.1	471	4 Q60730 homo sapien
12	168.5	21.1	498	4 Q60729 homo sapien
13	163.5	20.5	195	17 Q8ZX04 pyrobaculum
14	162.5	20.4	157	17 Q974T2 sulfobacillus
15	160.5	20.1	383	4 Q60728 homo sapien
16	160.5	20.1	594	4 Q9UNH5 homo sapien

17	160.5	20.1	623	4 Q60727 homo sapien
18	157.5	19.7	161	17 Q9VZ7 sulfolobus
19	159.1	19.1	151	17 Q9V1L1 Pyrococcus
20	151	18.9	553	5 Q9VW77 Pyrococcus
21	147.5	18.5	162	17 Q8UOC5 Pyrococcus
22	147.5	18.5	4	041711 homo sapien
23	146	18.3	146	17 Q93385 Pyrococcus
24	145.5	18.2	537	3 Q9PH11
25	143	17.9	446	5 Q9UX0
26	137.5	17.2	326	3 Q05673 saccharomyces cerevisiae
27	137	17.2	551	3 Q05180 saccharomyces cerevisiae
28	137	17.2	245	10 Q940J5 arabidopsis thaliana
29	137	17.2	337	10 Q92QPL arabidopsis thaliana
30	136	17.0	683	6 Q9RQ91 macaca fasciata
31	136	17.0	698	4 Q8Wx19 homo sapien
32	133	16.7	177	16 Q9RSG3 delinococcus
33	128.5	16.1	649	5 Q9V44 drosophila melanogaster
34	128	16.0	362	10 QRAUS9 oreaus onya sativa
35	125	15.7	419	2 Q07839 rhodobacter sphaeroides
36	124.5	15.6	542	3 Q9PBD4 candida albicans
37	123.5	15.5	752	4 Q9UE6 homosapiens
38	120	15.0	491	12 Q8QUP6 infectious agents
39	119	14.9	168	12 Q92506 bombyx mori
40	117	14.7	165	15 Q9Kt35 vibrio cholerae
41	116	14.5	168	12 Q9XKA4 oxaia mori
42	115	14.4	437	16 Q910U5 pseudomonas aeruginosa
43	115	14.4	463	10 Q9AJH9 oryza sativa
44	115	14.4	581	11 Q9DC11 ogaocci mus musculus
45	115	14.4	597	4 Q8WuN8 ogaocci mus musculus

ALIGNMENTS

RESULT 1

Q9BVJ7

PRELIMINARY;

PRT;

150 AA.

Q9BVJ7

DT

01-JUN-2001

(TREMBL)

17

Last sequence update

DT

01-DEC-2001

(TREMBL)

19

Last annotation update

DE

Hypothetical

protein

OS

homo sapiens

(Human)

Eukaryota

Metazoa

Chordata

Craniata

Vertebrata

Euteleostomi

OC

Mammalia

Eutheria

Primates

Cattarrhini

Hominoidea

OX

NCBI_TAXID:9606

RN

[1]

SEQUENCE FROM N.A.

RP

RC

TISSUE-LUNG

RA

Strausberg R

;

DR

Submitted

(DCC-2000)

to the

EMBL/GenBank/

DDJB

databases

.

DR

EMBL

BC00110

; AAH0140.1

; DR

InterPro

; IPR000340

; DS_phosphatase

DR

InterPro

; IPR00387

; TYR_phosphatase

DR

Pfam

; PF00782

; DSPC

; 1

DR

PROSITE

; PS00383

; TYR_phosphatase_1

DR

PROSITE

; PS00384

; TYR_phosphatase_2

DR

HYDROLASE

; Hypothetical

protein

DR

SEQUENCE

150 AA;

16588 NW;

4B72EFA0434B1B5F

CRC64;

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Db 121 ATAEIRRLRGSTIYEQEKAQFYQRTK 150
RESULT 2
 ID Q9W48 PRELIMINARY; PRY; 150 AA.
 AC Q9W48;
 DT 01-OCT-2000 (TREMbrel_15, Created)
 DT 01-OCT-2000 (TREMbrel_15, Last sequence update)
 DT 01-DEC-2001 (TREMbrel_19, Last annotation update)
 DE CDNA FLJ20442 f1s clone Kaf0482.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Watanabe K., Kumai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
 RA Suzuki Y., Ohayashi M., Nishi T., Shibahara T., Tanaka T.,
 RA Nakamura Y., Isogai T., Sugano S.;
 "NEDO human cDNA sequencing project.";
 Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 EMBL: AK000449; BA9172.1;
 DR InterPro; IPR00340; DS_phosphatase.
 DR InterPro; IPR00367; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR SMART; SM0012; PMPc_DSPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 150 AA; 16598 MW; 4B72E0D3D34B1B5F CRC64;
 Query Match 99.4%; Score 793; DB 4; Length 150;
 Best Local Similarity 99.3%; Pred. No. 5.7e-71;
 Matches 149; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGYQOPPNSWVLDGLPPLPAHQLFLDGLVRLVSLTERGPPPHSDSCPGTLHR 60
 Db 61 LRPDPGPAPPOIDDRYQIVDEBANARGEAVGHCAALGFGRGTGMALCYLVVERGLAGD 120
 QY 61 LRPDPGPAPPOIDDRYQIVDEBANARGEAVGHCAALGFGRGTGMALCYLVVERGLAGD 120
 Db 121 ATAEIRRLRGSTIYEQEKAQFYQRTK 150
 QY 121 ATAEIRRLRGSTIYEQEKAQFYQRTK 150
 Db 121 ATAEIRRLRGSTIYEQEKAQFYQRTK 150
RESULT 3
 ID Q9CW48 PRELIMINARY; PRY; 144 AA.
 AC Q9CW48;
 DT 01-JUN-2001 (TREMbrel_17, Created)
 DT 01-JUN-2001 (TREMbrel_17, Last sequence update)
 DE 130005N15RK protein (Fragment).
 GN 130005N15RK
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A. TISSUE=LIVER;
 NCBI_TAXID=10090;
 RX STRAIN=C57BL/6J;
 RX MEDLINE=2105650; PubMed=1217651;
 RX Kawai J., Shinagawa R., Shihata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa K., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann R., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Schriml L.W., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
 RA Guslincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchlioni L., Mashima J., Mazzarelli J., Mombberts P.,
 RA Nordone P., Rie B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynnshaw-Borik A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:655-690(2001).
 DR EMBL; AK04912; BAR23663.1; -.
 DR MGD; MGI:1915690; 130005N15RK.
 DR InterPro; IPR00387; TYR_phosphatase.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
 KW Hydrolase.
 FT NO+_TER 1 1
 DR SEQUENCE 144 AA; 16043 MW; ED7BA64AA8BE1052 CRC64;
 SQ Query Match 90.9%; Score 725; DB 11; Length 144;
 Best Local Similarity 94.4%; Pred. No. 3e-64; Mismatches 5; Indels 0; Gaps 0;
 Matches 136; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 7 NFSWVLDGLPPLPAHQLFLDGLVRLVSLTERGPPPHSDSCPGTLHR 126
 Db 61 CPPSPEQIQDFKVILDEANARGEAVGHCAALGFGRGTGMALCYLVVERGLAGD 60
 QY 1 NFSWVLDGLPPLPAHQLFLDGLVRLVSLTERGPPPHSDSCPGTLHR 126
 Db 61 CPPSPEQIQDFKVILDEANARGEAVGHCAALGFGRGTGMALCYLVVERGLAGD 60
RESULT 4
 ID P91585 PRELIMINARY; PRY; 190 AA.
 AC P91585;
 DT 01-MAY-1997 (TREMbrel_03, Created)
 DT 01-MAY-1997 (TREMbrel_03, Last sequence update)
 DE 01-DEC-2001 (TREMbrel_19, Last annotation update)
 DE COS41.7.
 OS Cliona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Asciidae; Enterogona;
 OC Phleobranchia; Clionidae; Cliona.
 RN NCBI_TAXID=7719;
 RP SEQUENCE FROM N.A.
 RA Bird A.P., Clark V.V., Jones S.J.M., Leitgeb S., Dobson R., Tweedie S.;
 DT 01-JUN-2000 (TREMbrel_2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98208558; PubMed=9539755;
 RA Siemann M.W., Leitgeb S., Clark V.H., Jones S.J.M., Bird A.;
 RT "Gene number in an invertebrate chordate, *Ciona intestinalis*.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:4437-4440(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9918102; PubMed=10024242;
 RA Siemann M.W., Leitgeb S., Charlton J., Jones S.J.M., Harris B.R.,
 RA Clark V.H., Bird A.;
 RT "Nonmethylated transposable elements and methylated genes in a
 RT chordate genome.";
 RT Science 283:1164-1167(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Siemann M.W., Bird A.;

"sequence analysis of transposable elements in the Sea Squirt, *Ciona intestinalis*"; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases. EMBL: 283760; CAB06051.1; - DRINTERPRO: IPR00340; DS_phosphatase. DRINTERPRO: IPR00387; TYR_phosphatase. SMART: SM00112; PPPC_DSPC; 1 PROSITE: PS00383; TYR_PHOSPHATASE_2; 1. SEQUENCE: 190 AA; 21292 MW; FB934267/DADAD27E CRC64;

Query Match

Best Local Similarity	Score	DB	Length	Matches	Pred.	No.	Score	Indels	Gaps
42.7%	242.5	5	190	61	Conservative	18	42.7%	25	39
					Mismatches				

RESULT 5

ID	AC	PPNFSWVPLGIGLAGLALPRLPAHOFLLGLGVRLHSITERGPSPHSDSCPGLTHRLRIP	DT	01-JUN-1998 (TREMBLrel. 06, Created)	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	DE	Hypothetical 76.7 KDa protein C17G10.4C in chromosome II.	GN	C17G10.4 or CDC14.	
OY	65	DFCPAPDQIDREVQIVDNEARANGEAVGHCALGRTGTMACLYVLRKGLAAGDAIE	Db	-----NQTVNETKSNNPKFGFVQAVAVHCAKGKISGIMLACYVVKMRKISAA	108	-----NQTVNETKSNNPKFGFVQAVAVHCAKGKISGIMLACYVVKMRKISAA	QY	125	IRRRLPGSSEIETYEQEKAYEQFYQ	147	160
Db	161	IRRRLPGSSEIETYEQEKAYEQFYQ	RR	[1]			RR	SEQUENCE FROM N.A.	RC	STRAIN=BRISTOL N2;	
RP	RN	Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.	RR	[2]			RR	REVISIONS.	RC	STRAIN=BRISTOL N2;	
RA	RL	Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.	RA	Waterston R.;	RN	[3]	RA	SEQUENCE FROM N.A.	RR	ERNSTING B.R., LI L., WISHART M.J., DIXON J.E.;	
RL	CC	Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.	RL	Bernsting B.R., Li L., Wishart M.J., Dixon J.E.;	CC	-1 ALTERNATIVE PRODUCTS: THE ORS C17G10.4A, C17G10.4B AND C17G10.4C REPRESENT PROBABLE ALTERNATIVE SPLICED FORMS OF A YET HYPOTHETICAL PROTEIN.	CC	-1 SIMILARITY: SOME TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. CDC14 SUBFAMILY.	CC	EMBL: 028739; AAB93458.1; -	
DR	DR	EMBL: AF000363; AAB94407.1; -	DR	EMBL: AF000363; AAB94407.1; -	DR	WormBase; C17G10.4C; CEB08288.	DR	WormBase; C17G10.4C; CEB08288.	DR	InterPro; IPR00340; DS_phosphatase.	
DR	DR	InterPro; IPR00387; TYR_phosphatase.	DR	InterPro; IPR00387; TYR_phosphatase.	DR	InterPro; IPR000242; Tyr_PP.	DR	InterPro; IPR000242; Tyr_PP.	DR	PRAM; PF00012; Y_Phasphatase; 1.	
DR	DR	PRAM; PF00012; Y_Phasphatase; 1.	DR	PRAM; PF00012; Y_Phasphatase; 1.	DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.	DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.	DR	PROSITE; PS00566; TYR_PHOSPHATASE_2; 1.	
KW	KW	HYPOTHETICAL PROTEIN; ALTERNATIVE SPlicing.	KW	HYPOTHETICAL PROTEIN; ALTERNATIVE SPlicing.	KW	SEQUENCE 681 AA; 16698 MW; 20056CDBFA03ADD CRC64;	KW	SEQUENCE 681 AA; 16698 MW; 20056CDBFA03ADD CRC64;	KW		

Query	Match	Score	DB	Length
OY	VOPPNFSWVGLGRAGLALPR-----LPAH-----YQFLDLCYVRHVL-----	23.4%	5	681
Db	VENGDFNWIIPGKILUSFCGPINESREBNGPYHAADVYFRENKVSTTVRNKAKYDA	29.8%	4	3e-10
OY	3 VOPPNFSWVGLGRAGLALPR-----LPAH-----YQFLDLCYVRHVL-----	29.8%	4	3e-10
Db	192 VENGDFNWIIPGKILUSFCGPINESREBNGPYHAADVYFRENKVSTTVRNKAKYDA	29.8%	4	3e-10
OY	43 ---TERGPPHSDCSPSLTHLRIRPDPCCPAPDQIDRFVQVDEANARGAEVGVHALGF	30;	49;	Mismatches
Db	252 SKFTKAGFDYD-----LFFTDGSTSDEIMKFIVKD--NTKG-GVAVICKAGL	30;	49;	Indels
OY	100 GRTGTMILACLYVKERGLAAGDAIAETRLRGSI---ETYEQEAKF	347	39;	Gaps
Db	300 GRTGTMILACWMKEYLTAGECMGWLVRVCRPCGSVIGPQQPYLIEQKF	347	7;	
RESULT 6				
P81299	PRELIMINARY;	PRT;	709 AA.	
ID				
AC	P81299;			
DR	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DE	Hypothetical 19.7 kDa protein C17G10.4 in chromosome 11.			
GN	C17G10.4.			
OS	Caenorhabditis elegans.			
OC	Bukay-Yota; Metzko; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OX	Rhabditidae; Pelorineriae; Caenorhabditis.			
RN	NCBI_TAXID=5239;			
[1]	SEQUENCE FROM N.A.			
RP	STRAIN=B-BRISTOL N2;			
RA	Johnson D.;			
RL	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.			
RN	{1}			
RP	REVISIONS.			
RC	STRAIN=B- BRISTOL N2;			
RA	Waterson R.;			
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1 ALTERNATIVE PRODUCTS: THE ORFS C17G10.4A, C17G10.4B AND C17G10.4C REPRESENT PROBABLE ALTERNATIVE SPLICED FORMS OF A YET HYPOTHETICAL PROTEIN.			
CC	-1 SIMILARITY: SOME, TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. CDCl4 SUBFAMILY.			
DR	EMBL: U28739; AB93457.1.			
DR	Wormpep; C17G10.4A; CE1656.			
DR	InterPro: IPR003440; DS_phosphatase.			
DR	InterPro: IPR00387; TIR_Phasphatase.			
DR	InterPro: IPR00242; TYR_PP.			
DR	PFam: PF00102; Y_phosphatase_1.			
DR	SMART: SM0012; PTPE_DSP; 1.			
DR	PROSITE: PS0033; TYR_PHOSPHATASE_1; 1.			
DR	PROSITE: PS5056; TYR_PHOSPHATASE_2; 1.			
KW	HYPOTHETICAL PROTEIN; Alternative Splicing.			
SQ	SEQUENCE 709 AA; 79739 MW; AB5873D8C7FEDB0C CRC64;			
Query	Match	23.4%	Score	186.5;
Best	Local Similarity	29.8%	DB	5;
Matches	50;	Conservative	Pred.	No. 4.5e-10;
Matches	50;	30;	Mismatches	49;
Matches	50;	30;	Indels	39;
Matches	50;	30;	Gaps	7;
OY	3 VOPPNFSWVGLGRAGLALPR-----LPAH-----YQFLDLCYVRHVL-----	29.8%	4	3e-10
Db	192 VENGDFNWIIPGKILUSFCGPINESREBNGPYHAADVYFRENKVSTTVRNKAKYDA	29.8%	4	3e-10
OY	43 ---TERGPPHSDCSPSLTHLRIRPDPCCPAPDQIDRFVQVDEANARGAEVGVHALGF	347	39;	
Db	252 SKFTKAGFDYD-----LFFTDGSTSDEIMKFIVKD--NTKG-GVAVICKAGL	347	7;	
OY	100 GRTGMLAYLVKERGLANGDAIAEIRRRLRIPDFCPAPDQIDRFVQVDEANARGAEVGVHALGF	299	99	
Db	300 GRTGMLAYLVKERGLANGDAIAEIRRRLRIPDFCPAPDQIDRFVQVDEANARGAEVGVHALGF	299	99	

Tue Nov 5 08:52:50 2002

us-09-619-380-2.rspt

Db 175 VENGDFNNIVPGKFLAFSPHPSKSIENGPYPLAPEAKFPYFKHNVTAVRLINKIYEA 234
Qy 43 --TERGPSPHSOCPGLLTHRLIPDCCPAPQIDREVQIVDEANARGEAVGHCALGF 99
Db 235 KRTTDAGGEHYD-----LIFDGSTPSDIVRRENLIE--NTEG-AIAVHCKAGL 282
Qy 100 GRGGTMLACYLVKERGLAAGDATAEIRRPGSI 133
Db 283 GRGGTLLACYVMHYRFTHAEITAWIRICRPSI 316

Search completed: November 4, 2002, 12:48:47
Job time : 84 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 4, 2002, 11:46:42 ; Search time 67 Seconds

Sequence: 1 MGVQPPNFSWVLPLAGLA.....GSIETYEQEKAVFQYQRTK 150 (without alignments)

Scoring table: BLOSUM62

Gpop 10.0 , Gapext 0.5

Searched: US-09-619-380-2

Perfect score: 798

Sequence: 1 MGVQPPNFSWVLPLAGLA.....GSIETYEQEKAVFQYQRTK 150

Scoring table: 298.322 Million cell updates/sec

Title: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002:

1: /SIDS2/gcgdata/geneseq/geneseq/geneseqP-emb1/AA11980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseq/geneseqP-emb1/AA11982.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseq/geneseqP-emb1/AA11983.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseq/geneseqP-emb1/AA11984.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseq/geneseqP-emb1/AA11985.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseq/geneseqP-emb1/AA11987.DAT:*

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8: /SIDS2/gcgdata/geneseq/geneseq/geneseqP-emb1/AA11990.DAT:*

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10: /SIDS2/gcgdata/geneseq/geneseq/geneseqP-emb1/AA11999.DAT:*

11: /SIDS2/gcgdata/geneseq/geneseq/geneseqP-emb1/AA119990.DAT:*

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21: /SIDS2/gcgdata/geneseq/geneseqP-emb1/AA2001.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseqP-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	798	100.0	150	22 AAB20328	Human protein phosphatase
2	798	100.0	150	22 AAB5275	Human dual specific phosphatase
3	798	100.0	179	23 ABB43078	Human ovarian anti-phosphatase
4	793	99.4	150	22 AAB73231	Amino acid phosphatase
5	793	99.4	150	22 AAG67453	Amino acid sequenc
6	793	99.4	150	22 AAG67632	Amino acid sequenc
7	793	99.4	150	23 ABB07846	Human tyrosine phos-
8	769	96.4	150	22 AAB73211	Murine phosphatase
9	764	95.7	150	22 AAB35276	Murine dual specific
10	186.5	23.4	681	23 ABB07847	C. elegans protein

ALIGNMENTS

RESULT 1

ID AAB20328 standard; Protein; 150 AA.

XX AAB20328;

XX DT 29-MAY-2001 (first entry)

XX DE Human protein phosphatase and kinase protein-7.

XX KW Protein phosphatase and kinase protein; PP1K7; human;

KW gastrointestinal disorder; immune system disorder;

KW neurological disorder; cell proliferative disorder; cancer;

KW diagnosis; therapy.

XX OS Homo sapiens.

XX FH Key Peptide Location/Qualifiers

FT FT FT FT FT FT

Protein Active-site Region

FT FT FT FT FT FT

/label= Signal_peptide

29..150 /label= Mature_protein

93..105 /note= "tyrosine specific protein phosphatase

/note= active site signature"

64..107 /note= "tyrosine phosphatase signature"

93..103 /note= "tyrosine specific protein phosphatase

/note= "tyrosine domain signature"

126..141 /note= "tyrosine specific protein phosphatase

/note= domain signature"

Amino acid sequence
Amino acid sequenc
Human dual specific
Human dual specific
Human dual specific
Human dual specific
Putative P. abyssi
Drosophila melanog
Arabidopsis thalia
Drosophila melanog
Arabidopsis MAPK p
Novel human diagno
Desulfovibrio aai
Human capping enzy
Human ORP872 phosp
Baculovirus RNA ba
RNA baculovirus ph
Human dual-specific
Human dual specific
Human dual specific
Human dual specific
Human dual specific
Novel human protei
Protein sequence o
Human protein phos
Human protein phos

PT Domain 74..125 "tyrosine specific protein phosphatase
PT /note= "domain signature"
PT 41
PT Modified-site 43
PT /note= "O-phosphorylated"
PT 7
PT Modified-site 7
PT /note= "N-glycosylated"
XX WO200120004-A2.
PN XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000; 2000WO-US25515.
XX
PR 15-SEP-1999; 99US-0154141.
XX
PA (INCYT) INCYTE GENOMICS INC.
YUE H, Tang YT, Bandman O, Hillman JL, Baughn MR, Azimzai Y;
PI Lu DAM;
PT XX
WPI: 2001-244811/25.
DR N-PSDB; AAF30482.
XX
PT Novel human protein phosphatase and kinase proteins for diagnosis,
PT treatment and prevention of gastrointestinal, immune system,
PT neurological and cell proliferative disorders -
XX
PS Claim 1; Page 91; 103pp; English.

XX
CC The present sequence is that of novel human protein phosphatase and
kinase protein PP HKP-7, as predicted from Incyte Clone ID No.
CC 1605974CBL (see AAF0482). Tissues that express PP HKP-7 (as a
fraction of total tissues expressing PP HKP-7) include reproductive
CC (0.372), cardiovascular (0.140) and endocrine (0.093). Diseases or
conditions associated with tissues expressing PP HKP-7 (as a
fraction of total tissues expressing PP HKP-7) include cancer
(0.558), inflammation or trauma (0.233) or cell proliferation
(0.209). The encoded protein shows homology to Cliona intestinalis
tyrosine phosphatase. The invention provides human PP HKP-1 to -11
peptides (see AAF304732) and poly nucleotides (see AAF304732).
It also provides expression vectors, host cells, antibodies, agonists
and antagonists, as well as methods for diagnosing, treating or
preventing disorders associated with expression of PP HKP, including
gastrointestinal disorders, immune system disorders, neurological
disorders and cell proliferative disorders, including cancer.

XX
SQ Sequence 150 AA;

Query Match 100.0%; Score 798; DB 22; Length 150;
Best Local Similarity 100.0%; Pred. No. 4.2e-85;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVOOPNFSWVLPGRLAGLALPRLAHYQPLLDGVRLVSLTERGPPHSDSCPGLTMR 60
1 MGVOOPNFSWVLPGRLAGLALPRLAHYQPLLDGVRLVSLTERGPPHSDSCPGLTMR 60

Db 61 LRIPDPFCPPAPRDQIDRFVQIVDEANARGAVGVHICALGFRGTGMLACLVKVERGLAAGD 120
61 LRIPDPFCPPAPRDQIDRFVQIVDEANARGAVGVHICALGFRGTGMLACLVKVERGLAAGD 120

QY 61 LRIPDPFCPPAPRDQIDRFVQIVDEANARGAVGVHICALGFRGTGMLACLVKVERGLAAGD 120
1 MGVOOPNFSWVLPGRLAGLALPRLAHYQPLLDGVRLVSLTERGPPHSDSCPGLTMR 60

Db 121 AIAEIRRRLPGSIEIYEQEKAQFQYRKT 150
121 AIAEIRRRLPGSIEIYEQEKAQFQYRKT 150

RESULT 3
ABP43078
ID ABP43078 standard; Protein; 179 AA.
XX
AC ABP43078;
XX
DT 22-AUG-2002 (first entry)

XX
DE Human ovarian antigen HVCAGJ27, SEQ ID NO:4210.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;

RESULT 2
AB35275
ID AAB35275 standard; Protein; 150 AA.
XX
AC AAB35275;
RC AAB35275;

QY	121	AIAEIRRRLRPGSITTYEQEKAQFQYQRTK	150
Db	121	AIAEIRRRLRPGPIETYEQEKAQFQYQRTK	150
RESULT	5		
ID	AAG67435		
XX			
AC	AAG67435;		
XX			
DT	26-NOV-2001	(first entry)	
XX			
DE	Amino acid sequence of a human polypeptide.		
XX			
KW	Human; protein kinase; protein phosphatase; signal transduction; intracellular signalling pathway.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200109345-A1.		
XX			
PD	08-FEB-2001.		
XX			
PF	28-JUL-2000; 2000WO-JP05060.		
XX			
PR	29-JUL-1999; 99JP-0248036.		
PR	18-OCT-1999; 99US-0159590.		
PR	11-JAN-2000; 2000US-0183322.		
PR	17-FEB-2000; 2000JP-018776.		
PR	02-MAY-2000; 2000JP-013567.		
PR	09-JUN-2000; 2000JP-0241899.		
PR	02-MAY-2000; 2000JP-0183767.		
XX			
PA	(HELI-) HELIX RES INST.		
XX			
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J, PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S; PI Senoo C, Nezu J;		
XX			
DR	WPI; 2001-564736/63.		
PT	New genes encoding protein kinase and protein phosphatase, useful for identifying modulators which can be used to treat human or animal disorders associated with the expression or function of these enzymes -		
PS	Example 4; Page 297-298; 336pp; Japanese.		
XX			
CC	The specification describes human protein kinase/protein phosphatases. The polypeptides are expected to participate in signal transduction in cells. The kinase/phosphatases are connected with intracellular signalling pathways. Antisense oligonucleotides and compounds identified by screening (agonists or antagonists) can be used to treat human or animal disorders associated with the expression or function of the protein. In addition, the polypeptides may be used as target molecules for drug development. The present sequence represents a polypeptide, used in the course of the invention.		
CC	Sequence 150 AA;		
SQ			
Query Match	99.4%	Score 793;	DB 22;
Best Local Similarity	99.3%	Pred. No. 1.6e-84;	Length 150;
Matches	149;	Conservative 0;	Mismatches 1;
		Indels 0;	Gaps 0;
QY	1	MGVQPPNFSWVLGRLAGLALPRLPAHQLFLDGLVRHLVSLTERGPPHSDSCPGTLHR	60
Db	1	MGVQPPNFSWVLGRLAGLALPRLPAHQLFLDGLVRHLVSLTERGPPHSDSCPGTLHR	60
QY	61	LRIPLDCPPADQDIDRFQVDEANARAEAVGHCALGFFGRTGTMALCYLVKERGLAED	120
Db	61	LRIPLDCPPADQDIDRFQVDEANARAEAVGHCALGFFGRTGTMALCYLVKERGLAED	120
QY	121	AIAEIRRRLRPGSITTYEQEKAQFQYQRTK	150
Db	121	AIAEIRRRLRPGPIETYEQEKAQFQYQRTK	150

RESULT 7

ID ABB07845 standard; Protein; 150 AA.

XX ABB07846:

DT 03-JUL-2002 (first entry)

DE Human tyrosine phosphatase-like enzyme.

XX Tyrosine phosphatase-like enzyme; antidiabetic; anorectic; cytostatic; cardiotonic; metabolic; immunomodulator; anti-parkinsonian; anticonvulsant; cerebroprotective; neuroprotective; nootropic; neuroleptic; anti-HIV; antiarrhythmic; hypotensive; vulnerary; gene therapy; human.

OS Homo sapiens.

XX

Key FH Region

FT 95..108

FT /note= "the encoding nucleotide fragment for the above residues is not indicated in the corresponding DNA sequence"

XX

PN WO20020747-A2.

PR 14-MAR-2002.

XX

PF 05-SEP-2001; 2001WO-EP10205.

XX

PR 11-SEP-2000; 2000US-231568P.

PR 06-DEC-2000; 2000US-251403P.

XX

PA (FARB) BAYER AG.

XX

PT Kossida S;

XX

PR WPI; 2002-339803/37.

DR N-PSDB; ABL40806.

XX

PT New human tyrosine phosphatase-like enzyme polypeptide, regulators of which are useful for preventing, treating diabetes, obesity, cancer, cardiovascular and pulmonary diseases

PR claim 18; FIG 2; 117pp; English.

CC The invention relates to a purified human tyrosine phosphatase-like enzyme polypeptide. The enzyme can be expressed by standard recombinant methodology. The tyrosine phosphatase-like enzyme and encoding polynucleotides are useful for screening for modulators which are used for treating a tyrosine phosphatase-like enzyme dysfunction related disease such as a central nervous system (CNS) disorder, diabetes, obesity, chronic obstructive pulmonary disease, cardiovascular disease, cancer, anorexia, cachexia, wasting disorders, appetite suppression, and other eating disorder such as bulimia. CNS disorders include brain injuries, Parkinson's disease, dementia, multiple sclerosis, stroke, Alzheimer's disease, Huntington's disease, schizophrenia, Pick's disease, Creutzfeldt-Jacobs dementia, progressive nuclear palsy, and human immunodeficiency virus (HIV) dementia, pain associated with CNS disorders and cardiovascular diseases include myocardial infarction, ischaemic diseases of the heart, atrial and ventricular arrhythmia, hypertensive vascular diseases and peripheral vascular diseases. The enzyme is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of mutations in the encoding nucleic acid sequences. The present sequence represents the human tyrosine phosphatase-like enzyme polypeptide.

XX Sequence 150 AA;

QY 1 MGVOPPNFSNVLPGLAGLALPRLPAHQLFLDGLGVRLHSVLTRGPPISDSCPGTLHR 60
1 MGVOPPNFSWVLPGRLAGLALPRLPAHQLFLDGLGVRLHSVLTRGPPISDSCPGTLHR 60

Db 61 LRIDFCPPADPODTRFYQIVDEANARAEAVYHCALFCRTGMLACLYLYKERGLAAGD 120
61 LRIPDFCPCPPADPODTRFYQIVDEANARAEAVYHCALFCRTGMLACLYLYKERGLAAGD 120

Db 121 ALAEIRRRLAPGSIETYEDEKAVQFYORTK 150
121 ALAEIRRRLAPGSIETYEDEKAVQFYORTK 150

RESULT 8

ID AAB73211 standard; Protein; 150 AA.

XX

AC AAB73211;

XX

DT 11-MAY-2001 (first entry)

DE Murine phosphatase AA023073-m.

XX

KW Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia; KW cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia; KW congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease; KW Moebius syndrome; Bjornstad syndrome; Bannayan-Zonana syndrome; KW schizophrenia; hamartoma.

OS Mus sp.

XX

PN WO200112819-A2.

XX

PR 22-FEB-2001.

XX

PA (SUGE-) SUGEN INC.

XX

PT 11-AUG-2000; 2000WO-US22158.

DR N-PSDB; AAF65563.

XX

PT New protein phosphatase polypeptide for diagnosing and treating PT phosphatase related disorders such as cancer, schizophrenia, cardiac dysfunction and/or vascular disorders

XX

PS Claim 6; FIG 5; 138pp; English.

CC The present invention relates to phosphatase proteins and coding CC sequences. The present sequence is one such phosphatase. Phosphatases are CC enzymes that catalyse the dephosphorylation of proteins modified by CC phosphorylation of serine, threonine or tyrosine residues. The CC phosphatases are useful for treating a variety of diseases, for example CC cancer e.g. breast, urogenital, prostate, head, neck, lung cancers, CC synovial sarcomas, renal cell carcinoma, non-small cell lung cancer, CC hepatocellular carcinoma, pancreatic endocrine tumours, stomach cancer, CC glioblastoma, colorectal cancer and thyroid cancer, pathophysiological CC hypoxia, cardiac dysfunction and/or vascular disorders, myopathies, CC congenital muscle disorders, Padior-Lefevre syndrome, Cowden disease, CC ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan CC Zonana syndrome, schizophrenia and hamartomas.

XX Sequence 150 AA;

QY 1 Query Match 99.4%; Score 793; DB 23; Length 150;
Best Local Similarity 99.3%; Pred. No. 1.e-81; Gaps 0;
Matches 149; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MGVOPPNFSWVLPGRLAGLALPRLPAHQLFLDGLGVRLHSVLTRGPPISDSCPGTLHR 60

Db	1 MGQOPPNFSWVLGRLAGLALPLPAHQLFLDGLVRHLVSLTERGPPHSDCGPLTHR	Db	121 AIAIRRRLRPGSETYEQKAVFQFYQRTK
QY	61 LRIPDFCPAPDQIDRFQIVDANARGEAVGHCALGFRGTCMMLACYLVKRGLAAGD	RESULT 10	
Db	61 MRIPDFCPSPSPEQIDQFVKIVDANARGEAVGHCALGFRGTCMMLACYLVKRGLAAGD	ID	ABB07847
QY	121 AIEIRRRLRPGSETYEQKAVFQFYQRTK	AC	ABB07847;
Db	121 AIAIRRRLRPGSETYEQKAVFQFYQRTK	XX	03-JUL-2002 (first entry)
• QY	150	XX	
RESULT 9	150	DE	C. elegans protein identified by EMBL Accession No.AF000363.
AAB35276	150	XX	Tyrosine phosphatase-like enzyme; antidiabetic; anorectic; cytostatic; carboxylant; metabolic; immunomodulator; antiparkinsonian; anticonvulsant; cerebroprotective; neuroprotective; nootropic; neuroleptic; anti-HIV; antiarrhythmic; hypotensive; pulmonary.
ID	150	XX	Caenorhabditis elegans.
XX	150	XX	W0200220747-A2.
AC	150	XX	PD 14-MAR-2002.
XX	150	XX	05-SEP-2001; 2001WO-EPI0205.
DT	08-MAY-2001 (first entry)	XX	PR 11-SEP-2000; 2000US-231568P.
DE	Murine dual specificity phosphatase DSP-11.	XX	PR 06-DEC-2000; 2000US-251403P.
XX	150	XX	PA (FARB) BAYER AG.
XX	150	XX	XX
XX	150	PI	Kossida S;
XX	150	XX	WPI; 2002-339803/37.
XX	150	DR	XX
XX	150	PT	New human tyrosine phosphatase-like enzyme polypeptide, regulators of which are useful for preventing, treating diabetes, obesity, cancer, cardiovascular and pulmonary diseases
XX	150	XX	PS Disclosure; Fig 3; 117P; English.
XX	150	XX	XX
XX	150	CC	The invention relates to a purified human tyrosine phosphatase-like enzyme polypeptide. The enzyme can be expressed by standard recombinant methodology. The tyrosine phosphatase-like enzyme and encoding polynucleotides are useful for screening for modulators which are used for treating a tyrosine phosphatase-like enzyme dysfunction related disease such as a central nervous system (CNS) disorder, diabetes, obesity, chronic obstructive pulmonary disease, cardiovascular disease, cancer, anorexia, cachexia, wasting disorders, appetite suppression, and other eating disorder such as bulimia. CNS disorders include brain injuries, Parkinson's disease, dementia, multiple sclerosis, stroke, Alzheimer's disease, Huntington's disease, schizophrenia, Pick's disease, Creutzfeldt-Jacob dementia, progressive nuclear palsy and human immunodeficiency virus (HIV) dementia, pain associated with CNS disorders and cardiovascular diseases include myocardial infarction, ischemic diseases of the heart, atrial and ventricular arrhythmia, hypertension and cardiovascular diseases and peripheral vascular diseases. The enzyme is useful in diagnostic assays for detecting diseases and abnormalities or mutations in the encoding nucleic acid sequences. The present sequence represents a C. elegans protein identified by EMBL Accn No.AF000363, used for alignment studies with the human tyrosine phosphatase-like enzyme polypeptide.
SQ	Sequence 150 AA:	XX	Sequence 681 AA;
Query Match	95.7%	Score 764; DB 22; Length 150;	Query Match 23.4%; Score 186.5; DB 23; Length 681;
Best Local Similarity	94.7%	Pred. No. 3.9e-81; Mismatches 3; Indels 0; Gaps 0;	Best Local Similarity 29.8%; Pred. No. 9.1e-13; Mismatches 50; Conservative 30; Mismatches 49; Indels 39; Gaps 7;
Matches	142;	CC	CC
Conservative	5;	CC	CC
Mismatches	3;	CC	CC
Indels	0;	CC	CC
Gaps	0;	CC	CC
• QY	1 MGQOPPNFSWVLGRLAGLALPLPAHQLFLDGLVRHLVSLTERGPPHSDCGPLTHR	Db	192 VENGFNWILPGKILSFCGPHNESREENQPYHADVVDFYRENKVSTIVRLNAKYDA
QY	61 LRIPDFCPAPDQIDRFQIVDANARGEAVGHCALGFRGTCMMLACYLVKRGLAAGD	QY	3 VOPENFSWTLGRLAGLALPLPAHQLFLDGLVRHLVSLTERGPPHSDCGPLTHR
Db	61 MRIPDFCPSPSPEQIDQFVKIVDANARGEAVGHCALGFRGTCMMLACYLVKRGLAAGD	Db	121 AIEIRRRLRPGSETYEQKAVFQFYQRTK
• QY	150	QY	150

QY 111 VKERGLAADAIAEIRRRLRPGSITVEGKAFQ-----FYQREK 150
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 300 MKHVRMATAETIAWRICRGLVIGPQQFLVMHQTSIMLEGDFYRQLK 349
 RESULT 13
 ID AAU75362
 ID AAU75362 standard; Protein; 578 AA.
 AC AAU75362;
 XX
 DE Human dual specificity phosphatase CDC14A deletion variant.
 XX
 DT 09-APR-2002 (first entry)
 KW Human; cell-cycle control; CDC14A; cancer; deletion variant;
 KW prostate cancer; breast cancer; tumour; lymph node metastasis;
 KW malignant mesothelioma; chromosome 1p21; dual specificity phosphatase;
 KW gene therapy; protein replacement therapy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 417..418
 PT /Note= "Wild-type RSDDTKRGHPRAVSQPFRL substituted by RL"
 XX US6331614-B1.
 PN US6331614-B1.
 XX
 PD 18-DEC-2001.
 XX
 PP 22-DEC-1999; 99US-0468872.
 XX
 PR 23-DEC-1998; 98US-113833P.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX
 PI Wong AKC, Teng DHF, Tavtigian SV;
 XX
 WPI; 2002-129551/17.
 DR N-PSDB; ABK13395.
 XX
 PT Nucleic acid encoding mutated form of human dual-specificity
 phosphatase CDC14A polypeptide, useful to diagnose and treat cancers -
 XX Example 1; Page -; 41pp; English.
 PS
 XX The invention relates to an isolated nucleic acid encoding a CDC14A
 CC polypeptide (cell-cycle control protein 14A, a dual specificity
 CC phosphatase), its complement or RNA molecule corresponding to it.
 CC Also included are an expression vector comprising the nucleic acid
 CC and a host cell transformed with the vector. The gene for CDC14A is
 CC located on human chromosome 1p21. The nucleic acid and protein are useful
 CC to diagnose and treat human cancers (e.g. breast cancer, prostate
 CC cancer) and tumours (e.g. lymph node metastasis, malignant mesothelioma)
 CC which have a mutation in the CDC14A gene, by gene therapy, protein
 CC replacement therapy or protein mimetics. They can also be used to
 CC screen for drugs to treat cancer. The present sequence represents a
 CC deletion variant of CDC14A encoded by a cDNA isolated from a breast cell
 CC line.
 Note: The present sequence is not shown in the specification but was
 CC created by the indexer using the CDC14A sequence appearing as AAU75361
 CC and the information in table 4.
 XX Sequence 578 AA;

QY 43 --TERGPPIRSDSCPGLTILRLRIDFCPPDIDPDRFOIVDARARAVGHCALGF 99
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 235 KRFTDAGEFHVD-----LFFIDGSTPSDNIVRFLINICE--NTEG-AIAVHKCAGL 282
 QY 100 GRTGMLACLVKERGLAADAIAEIRRRLPGSI 133
 DB 283 GRTGMLACLVKHYRTHAEIATIWRICRPGSI 316
 RESULT 14
 ID AAU75361
 ID AAU75361 standard; Protein; 594 AA.
 AC AAU75361;
 XX
 DT 09-APR-2002 (first entry)
 DE Human dual specificity phosphatase CDC14A.
 XX
 HH Human; cell-cycle control; CDC14A; cancer;
 KW prostate cancer; breast cancer; tumour; lymph node metastasis;
 KW malignant mesothelioma; chromosome 1p21; dual specificity phosphatase;
 KW gene therapy; protein replacement therapy.
 XX
 OS Homo sapiens.
 XX
 PN US6331614-B1.
 XX
 PD 18-DEC-2001.
 XX
 PP 22-DEC-1999; 99US-0468872.
 XX
 PR 23-DEC-1998; 98US-113833P.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX
 PI Wong AKC, Teng DHF, Tavtigian SV;
 XX
 WPI; 2002-129551/17.
 DR N-PSDB; ABK13392.
 XX
 PT Nucleic acid encoding mutated form of human dual-specificity
 phosphatase CDC14A polypeptide, useful to diagnose and treat cancers -
 XX PS Claim 1; Column 58-62; 41pp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a CDC14A
 CC polypeptide (cell-cycle control protein 14A, a dual specificity
 CC phosphatase), its complement or RNA molecule corresponding to it.
 CC Also included are an expression vector comprising the nucleic acid
 CC and a host cell transformed with the vector. The gene for CDC14A is
 CC located on human chromosome 1p21. The nucleic acid and protein are useful
 CC to diagnose and treat human cancers (e.g. breast cancer, prostate
 CC cancer) and tumours (e.g. lymph node metastasis, malignant mesothelioma)
 CC which have a mutation in the CDC14A gene, by gene therapy, protein
 CC replacement therapy or protein mimetics. They can also be used to
 CC screen for drugs to treat cancer. The present sequence represents a
 CC deletion variant of CDC14A.
 XX Sequence 594 AA;

QY 20 18; Score 160.5; DB 23; Length 594;
 Best Local Similarity 29.9%; Pred. No. 8.4e-10;
 Matches 46; Conservative 22; Mismatches 51; Indels 35; Gaps 5;

QY 3 VOPPNFSWTLPGRLA-----GLALPRPAHYQFLDLGVRLVSL----- 42
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 175 VENGDPMWVLPGRGLA-----GLALPRPAHYQFLDLGVRLVSL----- 234
 QY 43 --TERGPPIRSDSCPGLTILRLRIDFCPPDIDPDRFOIVDARARAVGHCALGF 99
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 235 KRFTDAGEFHVD-----LFFIDGSTPSDNIVRFLINICE--NTEG-AIAVHKCAGL 282
 QY 100 GRTGMLACLVKERGLAADAIAEIRRRLPGSI 133

Page 9

Db 235 KRFTDAGFEEHYD-----LFFIDGSPSDNTVRRFLNICE--NTEG-AIAVHCKAGL 282
 Qy 100 GRFTGMLACLYKVERGLAAGDAIAETRRLPGSI 133
 ||||| : ||| : ||| : ||| ||| |||
 Db 283 GRFTGMLACLYKVERGLAAGDAIAETRRLPGSI 316

Search completed: November 4, 2002, 12:46:16
Job time : 69 secs

Human dual specificity phosphatase CDCC14A G571R variant.
Human; cell-cycle control; DC14A; cancer; G571R;
prostate cancer; breast cancer; tumour; Lymph node metastasis;
malignant mesothelioma; chromosome 1p21; dual specificity phosphatase;
gene therapy; protein replacement therapy.

KEY
Misc-difference Location/Qualifiers
571
/note- "wild-type GLV substituted by Arg"

US6331614-B

18-DEC-2001

22-DEC-1999; 99US-0468872.

23-DEC-1998; 98US-113833P.

(MYRI-) MYRIAD GENETICS INC.

Wong AKC, Teng DHF, Tavtigian SV;

WPI; 2002-129551/17.
N-PGDB: ARK13387

ନୀଳେଖିଦ ପାତାର କହାଗଲିଏଇ ଯୁଦ୍ଧରେ ଫର୍ମା

phosphatase CBC1A polypeptide, use

Example 1; page -; 41pp; English.

The invention relates to an isolating arrangement, especially for central radiators.

The invention relates to an isolated nucleic acid encoding a CDC14A polypeptide (cell-cycle control protein 14A, a dual specificity phosphatase), its complement or RNA molecule corresponding to it, bis-inhibitors and compositions comprising them.

located on human chromosome 15q11-13.1 and encodes a host cell transformed with the vector. The gene for cdc14A is

to diagnose and treat human cancers (e.g., breast cancer, prostate cancer), and tumors (*i.e.*, lymph node metastases, malignant glioma).

which have a mutation in the CUC14A gene, by gene therapy, protein replacement therapy or protein inhibitors. They can also be used to

targeted for drugs to treat cancer. The present sequence represents a

Note: the present sequence is not shown in the specification but was created by the indexer using the CCDC14A sequence appearing as AAC175361

xx
SQ Sequence 594 AA;

Query Match 20.1%; Score 160.5; DB 23; Length 594;
 Best Local Similarity 29.9%; Pred. No. 8.4e-10;
 Matches 46; Conservative 22; Mismatches 51; Indexes 35; Gaps 5

43 --TERGPPPHSDSCPGILTHRLRIPDFCPAPDOIDRFVQIVDEANARGEAVGVHCALEF 999



CURRENT FILING DATE: 2000-12-29
 NUMBER OF SEQ ID NOS: 104
 SEQ ID NO: 95
 LENGTH: 196
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 FEATURE:
 NAME/KEY: DOMAIN
 OTHER INFORMATION: RNA triphosphatase domain of Drosophila melanogaster RNA capping enzyme
 US-09-752-165-95

Query Match 16.1%; Score 128.5; DB 4; Length 196;
 Best Local Similarity 28.6%; Pred. No. 5.2e-08; Matches 34; Conservative 22; Mismatches 42; Indels 21; Gaps 5; Length: 196
 SEQ ID NO: 93
 LENGTH: 195
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 NAME/KEY: DOMAIN
 OTHER INFORMATION: RNA triphosphatase domain of mammalian capping enzyme Mcel
 US-09-752-165-93

Query Match 14.4%; Score 115; DB 4; Length 195;
 Best Local Similarity 30.0%; Pred. No. 2.5e-06; Matches 24; Conservative 18; Mismatches 36; Indels 2; Gaps 1; Length: 195
 SEQ ID NO: 92
 LENGTH: 194
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 NAME/KEY: DOMAIN
 OTHER INFORMATION: RNA triphosphatase domain of xenopus laevis RNA capping enzyme
 US-09-752-165-92

Query Match 14.7%; Score 117.5; DB 4; Length 173;
 Best Local Similarity 25.7%; Pred. No. 1e-06; Matches 37; Conservative 19; Mismatches 51; Indels 37; Gaps 4; Length: 173
 SEQ ID NO: 91
 LENGTH: 173
 TYPE: PRT
 ORGANISM: Artificial/Unknown
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)..(173)
 OTHER INFORMATION: consensus sequence
 US-09-704-139-4

RESULT 3
 US-09-704-139-4
 Sequence 4, Application US/09704139
 ; GENERAL INFORMATION:
 ; APPLICANT: Kapeller, Rosanna
 ; TITLE OF INVENTION: A NOVEL DUAL SPECIFICITY PHOSPHATASE AND USES THEREFOR
 ; FILE REFERENCE: 10448-018001
 ; CURRENT APPLICATION NUMBER: US/09/704,139
 ; CURRENT FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: US 60/185,772
 ; PRIOR FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 4
 ; LENGTH: 173
 ; TYPE: PRT
 ; ORGANISM: Artificial/Unknown
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)..(173)
 ; OTHER INFORMATION: consensus sequence
 ; US-09-704-139-4

RESULT 4
 US-09-752-165-93
 Sequence 4, Application US/09752165
 ; GENERAL INFORMATION:
 ; APPLICANT: Shuman, Stewart
 ; PATENT NO.: 6451583
 ; TITLE OF INVENTION: For Treatment of Parasitic Infections
 ; FILE REFERENCE: D638B
 ; CURRENT APPLICATION NUMBER: US/09/752,165
 ; CURRENT FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 104
 ; SEQ ID NO: 96
 ; LENGTH: 195
 ; TYPE: PRT
 ; ORGANISM: Xenopus laevis
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; OTHER INFORMATION: RNA triphosphatase domain of xenopus laevis RNA capping enzyme
 ; US-09-752-165-96

Query Match 14.4%; Score 115; DB 4; Length 195;
 Best Local Similarity 30.0%; Pred. No. 2.5e-06; Matches 24; Conservative 18; Mismatches 36; Indels 2; Gaps 1; Length: 195
 SEQ ID NO: 95
 LENGTH: 194
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 NAME/KEY: DOMAIN
 OTHER INFORMATION: RNA triphosphatase domain of xenopus laevis RNA capping enzyme
 US-09-752-165-95

Query Match 14.4%; Score 115; DB 4; Length 195;
 Best Local Similarity 30.0%; Pred. No. 2.5e-06; Matches 24; Conservative 18; Mismatches 36; Indels 2; Gaps 1; Length: 195
 SEQ ID NO: 94
 LENGTH: 194
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 NAME/KEY: DOMAIN
 OTHER INFORMATION: RNA triphosphatase domain of xenopus laevis RNA capping enzyme
 US-09-752-165-94

RESULT 5
 US-09-752-165-96
 Sequence 96, Application US/09752165
 ; GENERAL INFORMATION:
 ; APPLICANT: Shuman, Stewart
 ; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
 ; FILE REFERENCE: D638B
 ; CURRENT APPLICATION NUMBER: US/09/752,165
 ; CURRENT FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 104
 ; SEQ ID NO: 96
 ; LENGTH: 195
 ; TYPE: PRT
 ; ORGANISM: Xenopus laevis
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; OTHER INFORMATION: RNA triphosphatase domain of xenopus laevis RNA capping enzyme
 ; US-09-752-165-96

Query Match 14.4%; Score 115; DB 4; Length 195;
 Best Local Similarity 30.0%; Pred. No. 2.5e-06; Matches 24; Conservative 18; Mismatches 36; Indels 2; Gaps 1; Length: 195
 SEQ ID NO: 95
 LENGTH: 194
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 NAME/KEY: DOMAIN
 OTHER INFORMATION: RNA triphosphatase domain of xenopus laevis RNA capping enzyme
 US-09-752-165-95

Query Match 14.4%; Score 115; DB 4; Length 195;
 Best Local Similarity 30.0%; Pred. No. 2.5e-06; Matches 24; Conservative 18; Mismatches 36; Indels 2; Gaps 1; Length: 195
 SEQ ID NO: 94
 LENGTH: 194
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 NAME/KEY: DOMAIN
 OTHER INFORMATION: RNA triphosphatase domain of xenopus laevis RNA capping enzyme
 US-09-752-165-94

RESULT 6
 US-09-134-218-4
 Sequence 4, Application US/09134218A
 ; GENERAL INFORMATION:
 ; APPLICANT: Shatkin, Aaron J.
 ; APPLICANT: Pillutla, Renuka
 ; APPLICANT: Reinberg, Danny
 ; APPLICANT: Yu, Zheng
 ; APPLICANT: Moldanado, Edic
 ; APPLICANT: Ho, C. Klong

TITLE OF INVENTION: mRNA CAPPING ENZYMES AND USES THEREOF
 FILE REFERENCE: 601-1-079 ss
 CURRENT APPLICATION NUMBER: US/09/134, 218A
 CURRENT FILING DATE: 1998-08-14
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 4 LENGTH: 597 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-134-218-4
 Query Match 14.4%; Score 115; DB 4; Length 597;
 Best Local Similarity 30.0%; Pred. No. 1.2e-05;
 Matches 24; Conservative 18; Mismatches 36; Indels 2; Gaps 1;
 Qy 69 PARQDQIDFVQIVDEANARG--EAVGVHCALGFRGTGMACLYK 126
 Db 98 PT'ENTENEFIRGERFNRSPPELIGVHCTHGNRTGFELICAFIVEKMDWSTEARAVATPA 157
 Db 158 QARPPGIKGDYKLKFRRY 177
 RESULT 7
 US-09-134-218-5
 Sequence 5, Application us/09134218A
 Patent No. 6312026
 GENERAL INFORMATION:
 APPLICANT: Shatkin, Aaron J.
 APPLICANT: Pillutla, Renuka
 APPLICANT: Reinberg, Danny
 APPLICANT: Yu, Zheng
 APPLICANT: Moldando, Edito
 TITLE OF INVENTION: mRNA CAPPING ENZYMES AND USES THEREOF
 FILE REFERENCE: 601-1-079 ss
 CURRENT APPLICATION NUMBER: US/09/134, 218A
 CURRENT FILING DATE: 1998-08-14
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 5 LENGTH: 597 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-134-218-5
 Query Match 14.4%; Score 115; DB 4; Length 597;
 Best Local Similarity 30.0%; Pred. No. 1.2e-05;
 Matches 24; Conservative 18; Mismatches 36; Indels 2; Gaps 1;
 Qy 69 PARQDQIDFVQIVDEANARG--EAVGVHCALGFRGTGMACLYK 126
 Db 98 PT'ENTENEFIRGERFNRSPPELIGVHCTHGNRTGFELICAFIVEKMDWSTEARAVATPA 157
 Db 158 QARPPGIKGDYKLKFRRY 177
 RESULT 8
 US-09-188-579-85
 Sequence 85, Application US/09188579B
 Patent No. 6107040
 GENERAL INFORMATION:
 APPLICANT: Shuman, Stewart
 TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
 FILE REFERENCE: D6185CIP/D
 CURRENT APPLICATION NUMBER: US/09/721, 362
 PRIOR APPLICATION NUMBER: US 09/315, 444
 PRIOR FILING DATE: 1999-05-20
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 85 LENGTH: 168 TYPE: PRT
 ORGANISM: baculovirus
 US-09-188-579-85
 Query Match 14.3%; Score 114; DB 3; Length 168;
 Best Local Similarity 32.6%; Pred. No. 2.7e-06;
 Matches 29; Conservative 13; Mismatches 43; Indels 4; Gaps 2;
 Qy 55 GLTLLRRLPDPFCPPAPPQDIDFVQIVDEANAR--EAVGVHCALGFRGTGMACLYKJ 112
 Db 77 GLYKKIQVPGQTLPESIIVEOFIDTVKBFTEKCPGMLVGVHCTHGINRTGYMVCYLMH 136
 Qy 113 ERGLAAAGDAIEIRRLRPSIE-TYE 139
 Db 137 TLGIAPOAEIDRFKARGHKIERONYVQD 165
 RESULT 9
 US-09-315-444-85
 Sequence 85, Application US/09315444A
 Patent No. 6232070
 GENERAL INFORMATION:
 APPLICANT: Shuman, Stewart
 TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
 FILE REFERENCE: D6185CIP/A
 CURRENT APPLICATION NUMBER: US/09/315, 444A
 CURRENT FILING DATE: 1999-05-20
 PRIOR APPLICATION NUMBER: US 09/188, 579
 PRIOR FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 85 LENGTH: 168 TYPE: PRT
 ORGANISM: baculovirus
 FEATURE:
 OTHER INFORMATION: Amino acid sequence of RNA baculovirus phosphatase BVP.
 US-09-315-444-85
 Query Match 14.3%; Score 114; DB 4; Length 168;
 Best Local Similarity 32.6%; Pred. No. 2.7e-06;
 Matches 29; Conservative 13; Mismatches 43; Indels 4; Gaps 2;
 Qy 55 GLTLLRRLPDPFCPPAPPQDIDFVQIVDEANAR--EAVGVHCALGFRGTGMACLYKJ 112
 Db 77 GLYKKIQVPGQTLPESIIVEOFIDTVKBFTEKCPGMLVGVHCTHGINRTGYMVCYLMH 136
 Qy 113 ERGLAAAGDAIEIRRLRPSIE-TYE 139
 Db 137 TLGIAPOAEIDRFKARGHKIERONYVQD 165
 RESULT 10
 US-09-721-362-85
 Sequence 85, Application US/09721362
 Patent No. 6420163
 GENERAL INFORMATION:
 APPLICANT: Shuman, Stewart
 TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
 FILE REFERENCE: D6185CIP/D
 CURRENT APPLICATION NUMBER: US/09/721, 362
 PRIOR APPLICATION NUMBER: US 09/315, 444
 PRIOR FILING DATE: 1999-05-20
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 85 LENGTH: 168 TYPE: PRT
 ORGANISM: baculovirus
 FEATURE:
 OTHER INFORMATION: Amino acid sequence of RNA baculovirus phosphatase BVP.
 US-09-721-362-85

Query Match, Score 14.3%; Best Local Similarity 32.6%; Pred. No. 2.7e-06; Number of Mismatches 29; Conservative 13; Indels 4; Gaps 2; Matches 31; Conservative 12; Mismatches 37; Indels 6; Gaps 3; Best Local Similarity 32.6%; Pred. No. 2.7e-06; Number of Mismatches 29; Conservative 13; Indels 4; Gaps 2; Matches 31; Conservative 12; Mismatches 37; Indels 6; Gaps 3;

RESULT 11
US-09-752-165-99
; Sequence 99, Application US/09752165
; Patent No. 6451583
; GENERAL INFORMATION:
; APPLICANT: Ho, C. Klong
; TITLE OF INVENTION: Pharmacological Targeting Of mRNA Cap Formation
; FILE REFERENCE: D6308
; CURRENT APPLICATION NUMBER: US/09/752,165
; NUMBER OF SEQ ID NOS: 104
; SEQ ID NO 99
; LENGTH: 168
; TYPE: PRT
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Baculovirus RNA-specific 5' phosphatase BVP

Query Match, Score 114; DB 4; Length 168;
Best Local Similarity 32.6%; Pred. No. 2.7e-06;
Matches 29; Conservative 13; Mismatches 43; Indels 4; Gaps 2; Matches 30; Conservative 11; Mismatches 26; Indels 8; Gaps 4; Score 114; DB 4; Length 168;
Best Local Similarity 32.6%; Pred. No. 2.7e-06; Number of Mismatches 29; Conservative 13; Indels 4; Gaps 2; Matches 31; Conservative 12; Mismatches 37; Indels 6; Gaps 3; Score 114; DB 4; Length 168;
Best Local Similarity 32.6%; Pred. No. 2.7e-06; Number of Mismatches 29; Conservative 13; Indels 4; Gaps 2; Matches 31; Conservative 12; Mismatches 37; Indels 6; Gaps 3;

RESULT 12
US-09-752-165-94
; Sequence 94, Application US/09752165
; Patent No. 6451583
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; APPLICANT: Ho, C. Klong
; TITLE OF INVENTION: Pharmacological Targeting Of mRNA Cap Formation
; FILE REFERENCE: D6308
; CURRENT APPLICATION NUMBER: US/09/752,165
; NUMBER OF SEQ ID NOS: 104
; SEQ ID NO 94
; LENGTH: 197
; TYPE: PRT
; ORGANISM: C elegans
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: RNA triphosphatase domain of C elegans RNA capping enzyme

Query Match, Score 14.3%; Best Local Similarity 32.6%; Pred. No. 2.7e-06; Number of Mismatches 29; Conservative 13; Indels 4; Gaps 2; Matches 31; Conservative 12; Mismatches 37; Indels 6; Gaps 3; Best Local Similarity 32.6%; Pred. No. 2.7e-06; Number of Mismatches 29; Conservative 13; Indels 4; Gaps 2; Matches 31; Conservative 12; Mismatches 37; Indels 6; Gaps 3; Best Local Similarity 32.6%; Pred. No. 2.7e-06; Number of Mismatches 29; Conservative 13; Indels 4; Gaps 2; Matches 31; Conservative 12; Mismatches 37; Indels 6; Gaps 3; Best Local Similarity 32.6%; Pred. No. 2.7e-06; Number of Mismatches 29; Conservative 13; Indels 4; Gaps 2; Matches 31; Conservative 12; Mismatches 37; Indels 6; Gaps 3;

RESULT 13
US-09-188-579-87
; Sequence 87, Application US/09188579A
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185
; CURRENT APPLICATION NUMBER: US/09/188,579B
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 87
; LENGTH: 173
; TYPE: PRT
; FEATURE:
; NAME/KEY: Candida albicans
; OTHER INFORMATION: Amino acid sequence of N-terminal RNA triphosphatase

Query Match, Score 114; DB 4; Length 173;
Best Local Similarity 40.0%; Pred. No. 4.9e-06;
Matches 30; Conservative 11; Mismatches 26; Indels 8; Gaps 4; Score 114; DB 4; Length 173;
Best Local Similarity 40.0%; Pred. No. 4.9e-06; Number of Mismatches 30; Conservative 11; Indels 8; Gaps 4; Score 114; DB 4; Length 173;
Best Local Similarity 40.0%; Pred. No. 4.9e-06; Number of Mismatches 30; Conservative 11; Indels 8; Gaps 4; Score 114; DB 4; Length 173;
Best Local Similarity 40.0%; Pred. No. 4.9e-06; Number of Mismatches 30; Conservative 11; Indels 8; Gaps 4; Score 114; DB 4; Length 173;

RESULT 14
US-09-315-444-87
; Sequence 87, Application US/09315444A
; Patent No. 6232070
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CIP
; CURRENT APPLICATION NUMBER: US/09/315,444A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/188,579
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 87
; LENGTH: 173
; TYPE: PRT
; FEATURE:
; NAME/KEY: Candida albicans
; OTHER INFORMATION: Amino acid sequence of N-terminal RNA triphosphatase

Query Match, Score 14.0%; Best Local Similarity 40.0%; Pred. No. 4.9e-06; Number of Mismatches 30; Conservative 11; Mismatches 26; Indels 8; Gaps 4; Score 112; DB 4; Length 173;
Best Local Similarity 40.0%; Pred. No. 4.9e-06; Number of Mismatches 30; Conservative 11; Mismatches 26; Indels 8; Gaps 4; Score 112; DB 4; Length 173;
Best Local Similarity 40.0%; Pred. No. 4.9e-06; Number of Mismatches 30; Conservative 11; Mismatches 26; Indels 8; Gaps 4; Score 112; DB 4; Length 173;
Best Local Similarity 40.0%; Pred. No. 4.9e-06; Number of Mismatches 30; Conservative 11; Mismatches 26; Indels 8; Gaps 4; Score 112; DB 4; Length 173;

Query Match, Score 14.2%; Best Local Similarity 36.0%; Pred. No. 4.4e-06; Number of Mismatches 30; Conservative 11; Mismatches 26; Indels 8; Gaps 4; Score 113; DB 4; Length 197;
; OTHER INFORMATION: RNA triphosphatase domain of C elegans RNA capping enzyme

Query Match, Score 14.2%; Best Local Similarity 36.0%; Pred. No. 4.4e-06; Number of Mismatches 30; Conservative 11; Mismatches 26; Indels 8; Gaps 4; Score 113; DB 4; Length 197;
; OTHER INFORMATION: RNA triphosphatase domain of C elegans RNA capping enzyme

QY 125 IRRURPGSIETVQE 139
| | :|:
| 154 FAENRQKGI--VKQD 166

RESULT 15
US-09-721-362-87

; Sequence 87, Application US/09721362

; Patent No. 6420163

; GENERAL INFORMATION:

; APPLICANT: Shuman, Stewart

; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation

; FILE REFERENCE: D6185CIP/D

; CURRENT APPLICATION NUMBER: US/09/721,362

; CURRENT FILING DATE: 2000-11-22

; PRIORITY NUMBER: US 09/315,444

; PRIOR FILING DATE: 1999-05-20

; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO: 87

; LENGTH: 173

; TYPE: PRT

; ORGANISM: Candida albicans

; FEATURE:

; OTHER INFORMATION: Amino acid sequence of N-terminal RNA triphosphatase

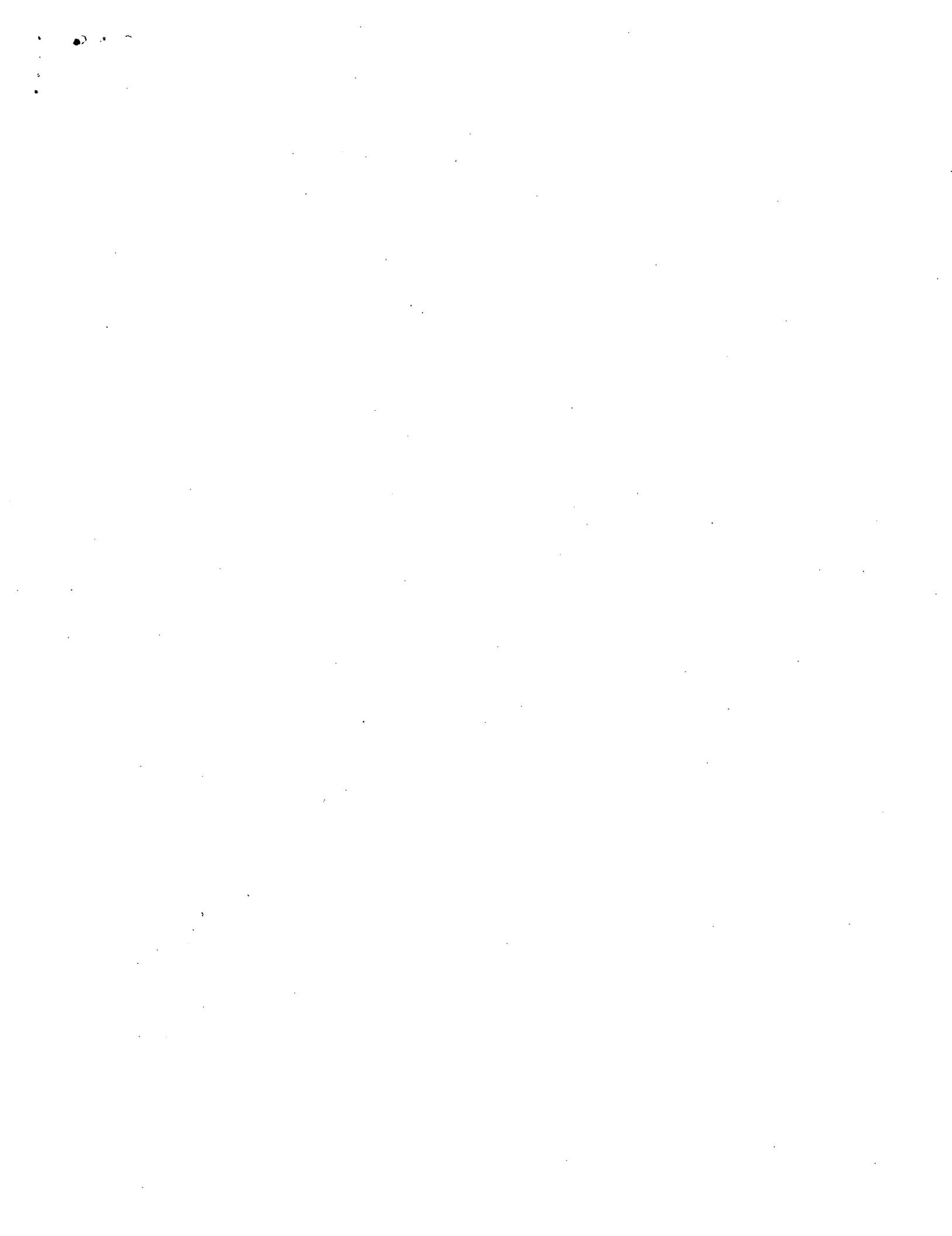
US-09-721-362-87

Query Match 14.0%; Score 112; DB 4; Length 173;
Best Local Similarity 40.0%; Pred. No. 4.96-06;
Matches 30; Conservative 11; Mismatches 26; Indels 8; Gaps 4;

QY 69 PAPDQIDRFVQTIDEANAR--GRAVGVHICALLSGTRGTGTMACVIL--VKERGLAAGDATAE 124
| :| |::| | :| ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 96 PROEDTDNFNIKVQEFRKYPDRVGVHCTHGFNRTGFLIAAXLFQVEEYGLDA--AIGE 153

QY 125 IRRURPGSIETVQE 139
| | :|:
Db 154 FAENRQKGI--VKQD 166

Search completed: November 4, 2002, 12:50:38
Job time : 28 secs



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OM protein - protein search, using sw model

Run on: November 4, 2002, 12:48:53 ; Search time 20 Seconds

(without alignments)

104.020 Million cell updates/sec

Title: US-09-619-380-2

Perfect score: 798

Sequence: 1 MGVQPPNFSWVLPGRLAGLA.....GSIEIVYEQEKAVFQFQRTK 150

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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11: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	117.5	147	173	US-09-816-494-7
2	117.5	173	10	Sequence 7, Appli
3	114	143	155	Sequence 4, Appli
4	114	143	517	Sequence 7, Appli
5	114	143	665	Sequence 21, Appli
6	114	143	665	Sequence 2, Appli
7	113.5	142	170	Sequence 26, Appli
8	113.5	142	170	Sequence 25, Appli
9	112	140	155	Sequence 6, Appli
10	111	139	172	Sequence 8, Appli
11	111	139	172	Sequence 5, Appli
12	110	138	201	Sequence 21, Appli
13	110	138	201	Sequence 7, Appli
14	107	134	157	Sequence 25, Appli
15	107	134	157	Sequence 10, Appli
16	106.5	133.5	156	Sequence 5, Appli
17	104	130	322	Sequence 14, Appli
18	104	130	595	Sequence 1, Appli
19	98	10	05-09-708-626-29	Sequence 29, Appli

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RESULT 1
US-09-816-494-7
; Sequence 7, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 2117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: consensus sequence
; OTHER INFORMATION: consensus sequence
US-09-816-494-7
Query Match 14.7%; Score 117.5; DB 10; Length 173;
Best Local Similarity 25.7%; Pred. No. 1.1e-05;
Matches 37; Conservative 19; Mismatches 51; Indels 37; Gaps 4;
QY 9 SWLPLGRLAGLAGLPRLPARYOFILDGLGRHLVSLTERCP-----PHSDSC 53
          | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: |
          Db 3 SETPHLPLIGSISTASENLALKKIGITIHWINVTEEPNPFLDKKKRNDRHNTAYSKN 62
          | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: |
          QY 54 PGITLHRIRIPDCCPAPDQI-----DRAFTVOLDEANARGAVGIVICAL 97
          | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: |
          Db 63 SGFTY-LQIPN---VDDHIYHIAWMHETKISKYFDEAVFIDARRQKGKVVLHGQA 116
          | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: |
          QY 98 GCGRTGTMILACYLKVKERGLAAGDA 121
          | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: | :||: |
          Db 117 GISRSATLITIAYLMKTRNLNEA 140
RESULT 2
US-09-815-419-4

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Sequence 2, Appli
Sequence 4, Appli
Sequence 24, Appli
Sequence 9, Appli
Sequence 3, Appli
Sequence 23, Appli
Sequence 8, Appli
Sequence 842, Appli
Sequence 18, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 28, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 3, Appli
Sequence 647, Appli
Sequence 22, Appli
Sequence 309, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 11, Appli

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; Sequence 4, Application US/09815419
; Patent No. US2002006406A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 18221, A NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 10448-030001
; CURRENT APPLICATION NUMBER: US/09/815,419
; CURRENT FILING DATE: 2001-03-22
; PRIORITY APPLICATION NUMBER: US 60/191,858
; PRIORITY FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: consensus sequence
; US-09-815-419-4

Query Match 14.7%; Score 117.5; DB 10; Length 173;
Best Local Similarity 25.7%; Pred. No. 1.1e-05; Mismatches 51; Indels 37; Gaps 4;
Matches 37; Conservative 19; Nucleotides 51; Indels 37; Gaps 4;

QY 9 SWYLPGRLAGLAPRLPAHYQFLIDGVRLYSITERGP-----PHSDSC 53
Db 3 SELPLHYGGSYSWAEAMALLLKLKGITHVINVTEEVNPFLDKKKNDRHYNAYTSKN 62

QY 54 PGTLHRKRPDPCCPAPDQI-----DRFVQVIDEANARGEVGVHIAL 97
Db 63 SGPTY--LQPNT---VDPHIVHIANNHETKISKYFDEAVDIDARQKGKVVLVHQQA 116

QY 98 GFRGTGTMACLYVKERGIAAGHA 121
Db 117 GISSRSATLIAVMKTRNLNEA 140

RESULT 3
US-09-964-277-7
; Sequence 7, Application US/09964277
; GENERAL INFORMATION:
; APPLICANT: Luchie, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; CURRENT FILING DATE: 2001-09-25
; PRIORITY FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-277-7

Query Match 14.3%; Score 114; DB 10; Length 155;
Best Local Similarity 26.4%; Pred. No. 2.2e-05; Mismatches 42; Indels 16; Gaps 3;
Matches 28; Conservative 20; Nucleotides 42; Indels 16; Gaps 3;

QY 50 SDSCPGGLT---HRLRIP---DFCPPADQIDRFQVIDEANARGEAVGVHICALGFR 102
Db 46 SNTCPKPDPDIPESHLFLRVYVNDSFCEKILPWLUDKSVDFTIEKAKASNGCVLVHCLAGISRS 105

QY 103 GIMLACLYVKERGIAAGDAIAETRLR-----GSIETYEQE 139
Db 106 ATTAIAVIMKRMDSLEAVRFVKEKPTISPNNFLGQQLDYEK 151

; RESULT 4
; Sequence 4, Application US/09815419
; Patent No. US2002006406A1
; GENERAL INFORMATION:
; APPLICANT: Luchie, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-277-21

Query Match 14.3%; Score 114; DB 10; Length 517;
Best Local Similarity 26.4%; Pred. No. 0.0001; Mismatches 42; Indels 16; Gaps 3;
Matches 28; Conservative 20; Nucleotides 42; Indels 16; Gaps 3;

QY 50 SDSCPGGLT---HRLRIP---DFCPPADQIDRFQVIDEANARGEAVGVHICALGFR 102
Db 44 SNTCPKPDPDIPESHLFLRVYVNDSFCEKILPWLUDKSVDFTIEKAKASNGCVLVHLAGISRS 103

QY 103 GTMLACLYVKERGIAAGDAIAETRLR-----GSIETYEQE 139
Db 104 ATTAIAVIMKRMDSLEAVRFVKEKPTISPNNFLGQQLDYEK 149

RESULT 5
US-09-816-494-2
; Sequence 2, Application US/09816494
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 2117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIORITY APPLICATION NUMBER: US 60/191,858
; PRIORITY FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-816-494-2

Query Match 14.3%; Score 114; DB 10; Length 665;
Best Local Similarity 26.4%; Pred. No. 0.00014; Mismatches 42; Indels 16; Gaps 3;
Matches 28; Conservative 20; Nucleotides 42; Indels 16; Gaps 3;

QY 50 SDSCPGGLT---HRLRIP---DFCPPADQIDRFQVIDEANARGEAVGVHICALGFR 102
Db 192 SNTCPKPDPDIPESHLFLRVYVNDSFCEKILPWLUDKSVDFTIEKAKASNGCVLVHCLAGISRS 251

QY 103 GTMLACLYVKERGIAAGDAIAETRLR-----GSIETYEQE 139
Db 252 ATTAIAVIMKRMDSLEAVRFVKEKPTISPNNFLGQQLDYEK 297

RESULT 6
US-09-964-277-2
; Sequence 2, Application US/09964277
; GENERAL INFORMATION:
; APPLICANT: Luchie, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-277-21

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; CURRENT APPLICATION NUMBER: US/09/964, 277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-277-2

Query Match      14.3%; Score 114; DB 10; Length 665;
Best Local Similarity 26.4%; Pred. No. 0.00014; Matches 28; Conservatiive 20; Mismatches 42; Indels 16; Gaps 3;
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY PHOSPHATASES
FILE REFERENCE: 200125_420
CURRENT APPLICATION NUMBER: US/09/775, 925
CURRENT FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-775-925-26

RESULT 7
US-09-775-925-26
; Sequence 26, Application US/09775925
; Patent No. US20010043358A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY PHOSPHATASES
; FILE REFERENCE: 200125_420
; CURRENT APPLICATION NUMBER: US/09/775, 925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-26

Query Match      14.3%; Score 114; DB 10; Length 665;
Best Local Similarity 23.9%; Pred. No. 0.00014; Matches 28; Conservatiive 20; Mismatches 42; Indels 16; Gaps 3;
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY PHOSPHATASES
FILE REFERENCE: 200125_420
CURRENT APPLICATION NUMBER: US/09/775, 925
CURRENT FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-775-925-26

RESULT 8
US-09-847-519A-11
; Sequence 11, Application US/09847519A.
; Patent No. US20020102693A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125_422
; CURRENT APPLICATION NUMBER: US/09/847, 519A
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-847-519A-11

Query Match      14.2%; Score 113.5; DB 10; Length 170;
Best Local Similarity 23.9%; Pred. No. 2.8e-05; Matches 37; Conservatiive 29; Mismatches 62; Indels 27; Gaps 5;
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY PHOSPHATASES
FILE REFERENCE: 200125_420
CURRENT APPLICATION NUMBER: US/09/775, 925
CURRENT FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-775-925-26

RESULT 9
US-09-964-277-6
; Sequence 6, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125_434
; CURRENT APPLICATION NUMBER: US/09/964, 277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-6

Query Match      14.0%; Score 112; DB 10; Length 155;
Best Local Similarity 24.8%; Pred. No. 3.7e-05; Matches 29; Conservatiive 25; Mismatches 43; Indels 20; Gaps 4;
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125_434
CURRENT APPLICATION NUMBER: US/09/964, 277
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 155
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-277-6

RESULT 10
US-09-816-494-8
; Sequence 8, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 2117, NOVEL DUAL SPECIFICITY PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816, 494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191, 858
; PRIOR FILING DATE: 2000-03-24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-816-494-8

Query Match      14.2%; Score 113.5; DB 10; Length 170;
Best Local Similarity 23.9%; Pred. No. 2.8e-05; Matches 37; Conservatiive 29; Mismatches 62; Indels 27; Gaps 5;
APPLICANT: Meyers, Rachel A.
APPLICANT: Luche, Ralf M.
TITLE OF INVENTION: 38692 AND 2117, NOVEL DUAL SPECIFICITY PHOSPHATASE MOLECULES AND USES THEREFOR
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816, 494
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-816-494-8

```

ORGANISM: Artificial Sequence
 FEATURE: Yue, Henry Guegler, Karl J.
 OTHER INFORMATION: consensus sequence Corley, Neil C.

US-09-816-494-8

Query Match Best Local Similarity 13.9%; Score 111; DB 10; Length 172;
 Matches 35; Conservative 22; Mismatches 51; Indels 34; Gaps 3;

QY 9 SWWLPGRLAGLAPRLPARYQFLIDLGVRHLVSLTERGPSPH---
 Db 3 SELPHYLGSYDASEANLALLKLKGTHVINVTEEVNNFELKKNDRYTNEYISKG 62

QY 100 GRGCTMIALCYLVVERGLAGDA 121
 Db 118 SRSATLVIAYLMTRNLSDA 139

RESULT 11

US-09-815-419-5

Sequence 5, Application US/09815419
 Patent No. US20020065406A1

GENERAL INFORMATION:
 APPLICANT: MEYERS, Rachel A.
 TITLE OF INVENTION: A NOVEL DUAL SPECIFICITY
 TITLE OF INVENTION: PHOSPHATASE AND
 TITLE OF INVENTION: USES THEREOF
 FILE REFERENCE: 1048-030001
 CURRENT APPLICATION NUMBER: US/09-815,419
 CURRENT FILING DATE: 2001-03-22
 PRIOR APPLICATION NUMBER: US 60/191,858
 PRIOR FILING DATE: 2000-03-24
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 172
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: consensus sequence

US-09-815-419-5

Query Match Best Local Similarity 13.9%; Score 111; DB 10; Length 172;
 Matches 35; Conservative 22; Mismatches 51; Indels 34; Gaps 3;

QY 9 SWWLPGRLAGLAPRLPARYQFLIDLGVRHLVSLTERGPSPH---
 Db 3 SELPHYLGSYDASEANLALLKLKGTHVINVTEEVNNFELKKNDRYTNEYISKG 62

QY 56 LTHLRLRIPDFEPPAQI-----
 Db 63 SGFTYQIOPNV----DDIYHIAWNTEKLSKYLEEAEVTFDAEKGGKVLYHCAGV 117

QY 100 GRGCTMIALCYLVVERGLAGDA 121
 Db 118 SRSATLVIAYLMTRNLSDA 139

RESULT 12

US-09-840-787-21

Sequence 21, Application US/09840787
 Patent No. US20020058264A1

GENERAL INFORMATION:
 APPLICANT: Lal, Preeti
 Hillman, Jennifer L.
 Bandman, Olga
 Shah, Purvi
 Au-Young, Janice

Yue, Henry Guegler, Karl J.
 Corley, Neil C.

TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
 NUMBER OF SEQUENCES: 98
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/840,787
 FILING DATE: 23-Apr-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/518,865
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0356 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 201 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 IMMEDIATE SOURCE:
 LIBRARY: CERVNOT01
 CLONE: 933353

SEQUENCE DESCRIPTION: SEQ ID NO: 21 :

US-09-840-787-21

Query Match Best Local Similarity 13.8%; Score 110; DB 10; Length 201;
 Matches 44; Conservative 25; Mismatches 61; Indels 28; Gaps 7;

QY 8 FSWLPGR-----LAGLALLRIPARYQFLIDLGVRHLVSLTERGPSPH---
 Db 25 FRGVKVPGRADRWHRIDTFVLG-ALPLRSLTQLVODENYRGVITNEETRFLCNS 83

QY 50 SDSCPGLUTLHLRIP--DFCP--PAPDQTDRYQIVDEANARGEAVGPHCALFGRTGTM 106

Db 84 SOEWRLGSEQLRLSTWMTGIGPTLDNLQKGVFALKYQSLGCVYVHKAGRGRSATM 143

QY 107 ACIVLKVERGLA--AGDIAEIR--RURPSIETYQ 138
 Db 144 AAYLIOVHKWSPEEAVALAKIRSYIHRRGGQDVLKE 181

RESULT 13

US-09-866-987-7

Sequence 7, Application US/09866987
 Patent No. US20020090703A1

GENERAL INFORMATION:
 APPLICANT: PLOMAN, GREGORY D.
 APPLICANT: MARTINEZ, RICARDO
 APPLICANT: WHITE, DAVID
 APPLICANT: MANNING, GERARD
 APPLICANT: SUDARSANAM, SUCHA
 APPLICANT: CAENEPEL, SEAN
 APPLICANT: HILL, RON

APPLICANT: FLANNAGAN, PETER
 TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
 FILE REFERENCE: 038602/1180
 CURRENT APPLICATION NUMBER: US/09/866, 987
 CURRENT FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: 60/208, 291
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 7
 LENGTH: 201
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: phosphatase polypeptide
 S-09-866, 987-7
 Query Match 13.8%; Score 110; DB 10; Length 201;
 Best Local Similarity 27.8%; Pred. No. 8.5e-05;
 Matches 44; Conservative 25; Mismatches 61; Indels 28; Gaps 7;
 APPENDIX: 8 FSWLWPLGR-----LAGALPRLPAHYQLLDGVRHLSLTERRGPPH---- 49
 b 25 FRGKVPGRAHRDWYHRIDPVTLIG ALPLRSLSITRQVQDENWRGVYTINNEEYETRFLCNS 83
 Y 50 SDSCPGLTLLRRIRIP---DFCP---PADDQDPRVOTVDEANARGEAVGVHCALGFGRTML 106
 b 84 SQEWKLRLGVEQLRUSTVDMTGIPTLDNLQKVOFALKYQSLGOCVYVHCKAGRSRSATMV 143
 Y 107 ACYLVKERGLA--RGDALEIR--RLRGSSEIYEQ 138
 b 144 AAYLIVLQHVKNMPEEAVRAIAKIRSYIHIRPGQDVLKE 181
 RESULT 14
 S-09-775-925-25
 Sequence 25, Application US/09775925
 Patent No. US20010049358A1
 GENERAL INFORMATION:
 APPLICANT: Lucche, Ralf M.
 APPLICANT: Wei, Bo
 TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
 FILE REFERENCE: 200125.420
 CURRENT APPLICATION NUMBER: US/09/775, 925
 CURRENT FILING DATE: 2001-02-01
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 25
 LENGTH: 157
 TYPE: PRT
 ORGANISM: Homo sapiens
 S-09-775-925-25
 Query Match 13.4%; Score 107; DB 10; Length 157;
 Best Local Similarity 25.5%; Pred. No. 0.00013;
 Matches 36; Conservative 25; Mismatches 56; Indels 24; Gaps 4;
 APPENDIX: 1 GATPPPPVGILRASFPVQILPNLYIGSA--RDSANLESIAKLGIRYIINVTPNLPNFEKNG 58
 Y 55 GLTRIRIPD-----FCPPADQDIDRFQIVDANARGEAVGVHCALGFGRTML 106
 b 90 Db 59 DEPHYKQPISDHSWQNSRFFEA-----IEFDIALSQNCGVLYHCLAGVSRSTVT 111
 QY 107 ACYLVKERGLAAGDATEIIRR 127
 b 112 VAYLMQKLHLISLNDAVDLVKR 132
 US-09-847-519A-10
 Query Match 13.4%; Score 107; DB 10; Length 157;
 Best Local Similarity 25.5%; Pred. No. 0.00013;
 Matches 36; Conservative 25; Mismatches 56; Indels 24; Gaps 4;
 APPENDIX: 2 GVPQPNES-----WLPGRLAGLAPRLPAHYQLLDGVRHLSLTERRGPPHSDSCP 54
 b 1 GATPPPPVGILRASFPVQILPNLYIGSA--RDSANLESIAKLGIRYIINVTPNLPNFEKNG 58
 Y 55 GLTRIRIPD-----FCPPADQDIDRFQIVDANARGEAVGVHCALGFGRTML 106
 b 90 Db 59 DEPHYKQPISDHSWQNSRFFEA-----IEFDIALSQNCGVLYHCLAGVSRSTVT 111
 QY 107 ACYLVKERGLAAGDATEIIRR 127
 b 112 VAYLMQKLHLISLNDAVDLVKR 132
 Search completed: November 4, 2002, 12:57:06
 Job time : 21 secs

RESULT 15

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES 8

ALIGNMENTS

AX078400
 LOCUS AX078400
 DEFINITION Sequence 1 from Patent WO0105983.
 ACCESSION AX078400
 VERSION AX078400.1
 KEYWORDS ;
 SOURCE human.
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 707)

Pred. No. is the number of results predicted by chance to have a

FEATURES	source	Ceptyr, Inc. (US)	AUTHORS	Toddendud,C.G., Bol,D., Finger,J., Lee,L., Nelson,T., Schlieven,G., Suchard,D.S., Banas,D., Bassolino,D., Feder,J.J., Kystek,S., Mcatee,P., Mintier,G., Siemers,N., Jackson,D.G. and Ramanathan,C.
BASE COUNT	ORIGIN	146 a /db_xref:"taxon:9606"	TITLE	Polynucleotides encoding human phosphatases
		224 c 202 g 135 t	JOURNAL	Patent: WO 02057460-A 151-25-JUL-2002; SQUIBB BRISTOL MYERS CO (US)
Query Match		100 %; Score 707; DB 6; Length 707;	Location/Qualifiers	1. .878
Best Local Similarity		100.0%; Pred. No. 5.6e-11;	/organism="Homo sapiens"	
Matches		707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/db_xref:"taxon:9606"	
QY	1	TGACCGCGCTGCGCCCTTGCCAGTGGGGGTGAGCCGCCAACTTCCTGG	/note="unnamed protein product"	89..541
Db	1	TGACCGCGCTGCGCCCTTGCCAGTGGGGGTGAGCCGCCAACTTCCTGG	/codon_start=1	
QY	61	GTGCCTCCSGGCCGCTGGGGACTGGCCCTGGGGGTGAGCCGCCAACTTCCTGG	/protein_id="CAD4455.1"	60
Db	61	GTGCCTCCSGGCCGCTGGGGACTGGCCCTGGGGGTGAGCCGCCAACTTCCTGG	/translation="MGVQIPNSWNLPLGRLAGLALPRLAHYOFLDGVYRHLVSLE	60
QY	121	CTGTTGGACCTGGGGTGCGCCACCTGGTGGCTGCGCCTGGGGGTGAGCCGCCAACTTCAGTC	RGPPIHSDSPGLIHLRKPDFCPAPDIDRFVQIVDEANAREAVSYHCAALGFR	120
Db	121	CTGTTGGACCTGGGGTGCAGCTGGCTGCGCCTGGGGGTGAGCCGCCAACTTCAGTC	GTMILACYLVERGLAAGDAIAEIRRRLPESIETEQEKAVQFQRTK"	120
QY	181	GACAGCTGCCGGCCTACCCCTGACCGCCTGCACATCCCAGCTTGCCCTGTTACCTGG	BASE COUNT	259 a
Db	181	GACAGCTGCCGGCCTACCCCTGACCGCCTGCACATCCCAGCTTGCCCTGTTACCTGG	247 c	233 g
QY	241	CCGACCGAGATGACGCCGCTTGCGAGATGCTGGAGGAGGCT	ORIGIN	139 t
Db	241	CCGACCGAGATGACGCCGCTTGCGAGATGCTGGAGGAGGCT	180	
QY	301	GTGGGAGTGCACCTGCGCTCGGGCTTGCGCCACTGGCACCACTGCTGGCTGTACCTG	Query Match	99.5%; Score 703.8; DB 6; Length 878;
Db	301	GTGGGAGTGCACCTGCGCTCGGGCTTGCGCCACTGGCACCACTGCTGGCTGTACCTG	Best Local Similarity	99.7%; Pred. No. 2.1e-116;
QY	361	GTGAGGAGGGGGCTGGAGAGAGGAGCATGCTGAACTGGACACTAGAACCC	Matches	705; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db	361	GTGAGGAGGGGGCTGGAGAGAGGAGCATGCTGAACTGGACACTAGAACCC	Db	59
QY	421	GGCTCCATCCGAGACCTATGAGCAGGAGAAGAGCAGCTTCCAGTGTACCTGGAGCAA	QY	61
Db	421	GGCTCCATCCGAGACCTATGAGCAGGAGAAGAGCAGCTTCCAGTGTACCTGGAGCAA	Db	119
QY	481	TAGGGGCCCTAGTACCTCTTACAGGCCCTACTCCCTTCCCATGTTGATGG	QY	121
Db	481	TAGGGGCCCTAGTACCTCTTACAGGCCCTACTCCCTTCCCATGTTGATGG	Db	119
QY	541	GCAGAGATGAGGAGGAGCTGAGTAAGTTAACCCCTTAGCCTCCATGTTGAGA	QY	179
Db	541	GCAGAGATGAGGAGGAGCTGAGTAAGTTAACCCCTTAGCCTCCATGTTGAGA	Db	181
QY	601	CACTGAGTAGGCCAACCCCTGCGAGCAGGTCCATTGAGGGAGGTGACTGCTT	QY	241
Db	601	CACTGAGTAGGCCAACCCCTGCGAGCAGGTCCATTGAGGGAGGTGACTGCTT	Db	29
QY	661	GTGTTAAATGAGTTAGGACCAAAAAAA	QY	301
Db	661	GTGTTAAATGAGTTAGGACCAAAAAAA	Db	419
RESULT 2			GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	360
AX482482	AX482482	878 bp DNA	GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	358
LOCUS	Sequence	151 from Patent WO02057460.	Db	421
DEFINITION			GGCTCCATCCGAGACCTATGAGCAGGAGAAGAGCAGCTTCCAGTGTACCTGG	418
ACCESSION	AX482482		GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	420
VERSION	AX482482.1	GI:22317003	Db	419
SOURCE	human.		GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	478
ORGANISM	Homo sapiens		GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	480
REFERENCE	1	Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.	Db	479
			GGCTCCATCCGAGACCTATGAGCAGGAGAAGAGCAGCTTCCAGTGTACCTGG	538
			GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	540
			GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	598
			GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	599
			GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	600
			GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	658
			GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	660
			GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	718
			GTGAGGAGGGGGCTTGCGAGAGATGCTGGAGGAGGCT	719

Db	303	CAGGCTGGCCGTACTCTGGTAANGAGGAGCGGGNGCTGGCTGAGGAGATGCCATTGCTG	362	/clone="IMAGE:358809" /clone_1.lib="Soares_fetal_heart_NbHH19W"
Qy	401	AAATCGGACGACTACGACCCGCTCATCGAGACCTATGAGCAGGAGAACCGAGTCTTC	460	54. .339 /note="similar to Cliona intestinalis protein 283760 (PID:91764017)"
Db	363	AAATCGGACGACTACGACCCGCTCATCGAGACCTATGAGCAGGAGAACCGAGTCTTC	422	misc_feature 61. .330 /note="similar to Homo sapiens protein AF064105 (PID:93136334)"
Qy	461	AGPTCACCAGGAAGAATAAGGGCCTTAGTACCCCTACAGGCCCTACTCCCC	520	482 misc_feature 85. .333 /note="similar to Pyrococcus horikoshii protein AB009524 (PID:93132001)"
Db	423	AGTTCATGACCGAGGAAGAAATAGGGCCTTAGTACCCCTACAGGCCCTACTCCCC	580	580 misc_feature 91. .297 /note="similar to Caenorhabditis elegans protein U28739 (PID:92731378)"
Qy	521	TTCGGATGTTGCGATGGCCAGATGAGGAGGAGTGAAGTAAAGTAAACCTC	542	91. .297 /note="similar to Homo sapiens protein 283760 (PID:93136334)"
Db	483	TTCGGATGTTGCGATGGCCAGATGAGGAGGAGTGAAGTAAACCTC	640	602 misc_feature 91. .297 /note="similar to Caenorhabditis elegans protein U28739 (PID:92731379)"
Db	543	TAGCTCCATGCTGAGACACTGAAGTAGCCCCACCCCTGAGGCAGSTCTGATTGAA	602	
RESULT 12				
LOCUS	HUMZEL2H05	559 bp mRNA linear. PRI 29-AUG-1998		
DEFINITION	Homo sapiens full length insert cDNA clone ZE12H05.			
ACCESSION	AF086553			
VERSION	AF086553.1			
KEYWORDS	FLI, CDNA.			
SOURCE	Homo sapiens.			
ORGANISM				
REFERENCE				
AUTHORS	Woesner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,			
MARTH,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B.,				
Gelsel,S., Allen,M., Underwood,K., Chappell,J., Person,B.,				
Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,				
Schurk,R., Ritter,E., Kohn,S., Shaller,T., Behymer,K., Hillier,L.,				
Wilson,R. and Waterston,R.				
TITLE	Full Clone Sequencing of the Longest Available Member from Each			
JOURNAL	Unigene Cluster			
REFERENCE	Unpublished			
AUTHORS	Waterston,R.			
JOURNAL	Direct Submission			
COMMENT	Submitted (24-AUG-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA			
SUBMITTED BY:	Genome Sequencing Center			
Department of Genetics				
Washington University				
St. Louis MO 63108, USA				
http://genome.wustl.edu/gsc				
mailto:est@watson.wustl.edu				
NOTICE: This sequence represents the full insert of this cDNA. NO attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.				
SIMILARITY INFORMATION:				
Similar to Cliona intestinalis protein Z83760 (PID:91764017) cos41.7				
FEATURES	The location of this clone is unknown.			
source	Location/Qualifiers			
	I. .559			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
RESULT 13				
LOCUS	AX39838	553 bp DNA linear	PAT 27-MAY-2002	
DEFINITION	Sequence 9 from Patent WO020747.			
ACCESSION	AX39838			
VERSION	AX39838.1			
KEYWORDS				
SOURCE	human.			

ORGANISM	Homo sapiens	Regulation of human tyrosine phosphatase-like enzyme
EUKARYOTA;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Patent: WO 0220747-A 5 14-MAR-2002;
MAMMALIA;	Eutheria; Primates; Catarrhini; Hominidae; Homo.	Bayer Aktiengesellschaft (DE)
REFERENCE	Kossida, S.	Location/Qualifiers
AUTHORS		1..493
JOURNAL	Regulation of human tyrosine phosphatase-like enzyme	
PATENT	WO 0220747-A 5 14-MAR-2002;	
FEATURES	Bayer Aktiengesellschaft (DE)	
SOURCE	/organism="Homo sapiens"	
BASE COUNT	96 a 186 c 168 g 103 t	/db_xref="taxon:9606"
ORIGIN		
Query Match	71.9%; Score 508.6; DB 6; Length 553;	
Best Local Similarity	98.6%; Pred. No. 1..9e-81;	
Matches	555; Conservative 0; Mismatches 4; Indels 4; Gaps 3;	
Db	1 CGATGGCGCTGAGCCCCCACTCTCTGGTGTGGACTGGCGCTGGGGACCTGG 88	
Qy	89 CGCTGGCGGGCTCCCGCCCATACAGTTCTGTGACCTGGCAGCTGGCGTGGGGACCTGG 148	
Db	61 CGCTGGCCCGGGCTCCCGCCCATACAGTTCTGTGACCTGGCAGCTGGCGTGGGGACCTGG 120	
Qy	149 TGTCTCTGAC-GGAGCGGGGCCCTCACGGACAGCTGCCCGGCTTACCCCTGA 206	
Db	121 TGTCTCTGACCTGGAGCTGGGGGCCCTCACAGGACAGCTGCCCGGCTTACCCCTGA 180	
Qy	207 CGCTCTGGCATCCC-GACTCTGGCCGGCCCTACCTGGCTCTGGTGTGGACTCTGGC 265	
Db	181 CGCCTCTGGCATCCCCTGACTCTGGCCGGCCGGCCGACAGATCGACCGCTGGTC 240	
Qy	266 AGATCTGGACAGA-GGCCAACCCACGGGAGAGGCTGTGGAGTGCCTCTGGC 324	
Db	241 AGATCTGGACAGA-GGCCAACCCACGGGAGAGGCTGTGGAGTGCCTCTGGC 300	
Qy	325 TTGGCCGCACTGGCACCATGCTGGCTTACCTGGTGAAGGAGCGGGCTTGCTGA 384	
Db	301 TTGGCCGCACTGGCACCATGCTGGCTTACCTGGTGAAGGAGCGGGCTTGCTGA 360	
Qy	385 GAGATGGCATCTGTAATTCGAGACTACGACCCGCTCACAGACCTATGAGSCAG 444	
Db	361 GAGATGGCATCTGTAATTCGAGACTACGACCCGCTCACAGACCTATGAGSCAG 420	
Qy	445 GAGAAAGAGCTCTTCCAGCTTACCGAGAACCAAATAGGSCCTTGTACCTTCAC 504	
Db	421 GAGAAAGAGCTCTTCCAGCTTACCGAGAACCAAATAGGSCCTTGTACCTTCAC 480	
Qy	505 CAGGCCCTCACCTCCCTGGCTGTCAGTGGGCCAGAGATGAGGGAGTGGACT 564	
Db	481 CAGGCCCTCACCTCCCTGGCTGTCAGTGGGCCAGAGATGAGGGAGTGGACT 540	
Qy	565 AAAGTATTAACC 577	
Db	541 AAAGTATTAACC 553	
RESULT	14	
AJ398834	AJ398834 493 bp DNA linear PAT 27-MAY-2002	
LOCUS		
DEFINITION	Sequence 5 from Patent WO0220747.	
ACCESSION	AJ398834	
VERSION	AJ398834.1 GI:21261346	
KEYWORDS	human.	
SOURCE		
ORGANISM	Homo sapiens	
EUKARYOTA;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
MAMMALIA;	Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	Kossida, S.	
AUTHORS		
JOURNAL	Regulation of human tyrosine phosphatase-like enzyme	
PATENT	WO 0220747-A 10 14-MAR-2002;	
FEATURES	Bayer Aktiengesellschaft (DE)	
SOURCE	/organism="Homo sapiens"	
BASE COUNT	93 a 112 c 120 g 103 t	/db_xref="taxon:9606"
ORIGIN		
RESULT	15	
AJ398839	AJ398839 448 bp DNA linear PAT 27-MAY-2002	
LOCUS		
DEFINITION	Sequence 10 from Patent WO0220747.	
ACCESSION	AJ398839	
VERSION	AJ398839.1 GI:21261351	
KEYWORDS	human.	
SOURCE		
ORGANISM	Homo sapiens	
EUKARYOTA;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
MAMMALIA;	Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	Kossida, S.	
AUTHORS		
JOURNAL	Regulation of human tyrosine phosphatase-like enzyme	
PATENT	WO 0220747-A 10 14-MAR-2002;	
FEATURES	Bayer Aktiengesellschaft (DE)	
SOURCE	/organism="Homo sapiens"	
BASE COUNT	93 a 112 c 120 g 103 t	/db_xref="taxon:9606"
ORIGIN		
RESULT	16	
AJ398839	AJ398839 448 bp DNA linear PAT 27-MAY-2002	
LOCUS		
DEFINITION	Sequence 10 from Patent WO0220747.	
ACCESSION	AJ398839	
VERSION	AJ398839.1 GI:21261351	
KEYWORDS	human.	
SOURCE		
ORGANISM	Homo sapiens	
EUKARYOTA;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
MAMMALIA;	Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	Kossida, S.	
AUTHORS		
JOURNAL	Regulation of human tyrosine phosphatase-like enzyme	
PATENT	WO 0220747-A 10 14-MAR-2002;	
FEATURES	Bayer Aktiengesellschaft (DE)	
SOURCE	/organism="Homo sapiens"	
BASE COUNT	93 a 112 c 120 g 103 t	/db_xref="taxon:9606"
ORIGIN		

Query Match	Score	DB	Length
Best Local Similarity	100.0%	pred.	No. 3-1e-0
Matches	446	Conservative	0
Indels	0	Mismatches	0
Gaps			
241 CCCGAGCAGAGCGACCGCTTGTGAGATCTGGACGAGGCCAACCCACGGGAGAGCT	300		
448 CCGCACCAGCATGCACGCCCTGTCAGATCTGGACGAGGCCAACCCACGGGAGAGCT	389		
301 GTGGGAGTGCCTGTCCTGGCTTGCGCGACTGGCACATGCTGGCTGTGTACCTG	360		
388 GTGGGAGTGCCTGTCCTGGCTTGCGCGACTGGCACATGCTGGCTGTGTACCTG	329		
361 GTGAAAGGAGCGGGCTTGGCGAGGATGCCATGCTGAATCCGACGAGCTACGACC	420		
328 GTGAAAGGAGCGGGCTTGGCTGCAGGAGATGCCATGCTGAATCCGACGAGCTACGACC	269		
421 GGCTCCATGAGACCTATGACGAGGAGAACGAGCTTCAGTTCAACAGGAA	480		
268 GGCTCCATGAGACCTATGACGAGGAGAACGAGCTTCAGTTCAACAGGAA	209		
481 TAAGGGCCCTTAGTACCTCTTACAGGCCCTACGCCCTTCCCCTGTCGATGG	540		
208 TAAGGGCCCTTAGTACCTCTTACAGGCCCTACGCCCTTCCCCTGTCGATGG	149		
541 GCCAGAGATGAGGGAGTGCCTAAGTAAACCTCTAGCTCCATTGGCTGAGA	600		
148 GGCAGAGATGAGGGAGTGCCTAAGTAAACCTCTAGCTCCATTGGCTGAGA	89		
601 CACTGAGTAGGCCACCCCTCAGGGAGTCTGTGAGAAGGGAGCTTACTGCTT	660		
88 CACTGAGTAGGCCACCCCTCAGGGAGTCTGTGAGAAGGGAGCTTACTGCTT	29		
661 GTTGTATAATGAGTTTACGACCA	686		
28 GTTGTATAATGAGTTACGACCA	3		

Search completed: November 4, 2002, 08:49:28
Job time : 2789 secs

Page
2

mitogen-activated protein kinase, is used to identify agents inhibiting the enzyme activator and modulate cell proliferation.

29-MAY-2001 (first entry)
Human protein phosphatase and kinase protein-7 cDNA 100697CBL.
Protein phosphatase and kinase protein; PPHKBP-7; human;
gastrointestinal disorder; immune system disorder;
neurological disorder; cell proliferative disorder; cancer;
diagnosis; therapy; ss.

CC KX
human DSP-11 coding sequence.

Key
CDS
homo sapiens.

Location/Qualifiers
104::556

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Query Match          100.0%; Score 707; DB 22; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.9e-138;
Matches 707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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sig_peptide    /tag= 104-187  
mat_peptide   /tag= b 188-553  
/*tag= c
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misc_feature  
251..310  
/tag=d  
/note= "unique fragment"
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bb	61	GTTGCTTCCGGGCGGCTGGGAGCTGGCTGCCTGCCGCGCCTCCGGCCCACTACAGTC	120
YY	121	CTGTGNGACCCTGGCGCTGGCGCACCTGGTGTGACTCTGAGGGAGCGGGCCCTCACAGC	180

22-MAR-2001.

15-SEP-1999; 990US-0154141.
(INCY-) INCYTE GENOMICS INC.

161 GACAGCTGCGCCGCTTACCGTGACGGCAGGCAACGCTGGCCGGCC 240
 241 CGCGGAGGAGGAGGCGCTTGTCGACATCGTGACGGCCAGCAGGCGAGS 300.

Yue H., Tang YT, Bandman O, Hillman JL, Baughn MR, Azimzai Y
Lu DAM;
warr. 2001-24491/25

F-RSUS: AAC20328. Novel human protein phosphatase and kinase proteins for diagnostic treatment and prevention of gastrointestinal, immune system,

Claim 5; Page 99-100; 103PP; English.

Y	421	GGCTCCATCGAGACCTATGAGAGAGAAGAGCTTCAGCTTCCAGGTCTTACCGCGAACGAA	480
	421	GGCTCCATCGAGACCTATGAGAGAGAAGAGCTTCAGCTTCCAGGTCTTACCGCGAACGAA	480
b	421	GGCTCCATCGAGACCTATGAGAGAGAAGAGCTTCAGCTTCCAGGTCTTACCGCGAACGAA	480

protein phosphatase and kinase protein PP HKP-7 (see NAB031628). The cDNA was initially identified in Incyte PP HKP-7 clone (ID 130628). Tissue from an adult lung tissue library. Tissues that express PP HKP-7 include a fraction of total tissues examined (n=12).

Y	TAAGGGCCCTTAGTACCCCTTGATCCGCCCCACTCCGCCCTTCAGTGTGCGAAGGG	540
b	TAAGGGCCCTTAGTACCCCTTGATCCGCCCCACTCCGCCCTTCAGTGTGCGAAGGG	540

reproductive (0.3%), cardiovascular (0.14%) and endocrine (0.09%) diseases (as a fraction of total tissues expressing PIPK-7), include cancer (0.558), inflammation or trauma (0.233) or cell proliferation (0.233).

Y
 b
 541 GCCAGAGATGAGGGAGTGCCTAAAGTAATTAACCTCTTCAGCTCCATGGCTGAGA 600
 541 GCCAGAGATGAGGGAGTGCCTAAAGTAATTAACCTCTTCAGCTCCATGGCTGAGA 600

tyrosine phosphatase. The invention provides human PTK111 to polypeptides (see AB20322-32) and poly nucleotides (see AF303772). It also provides expression vectors, host cells, antibodies, agonists,

preventing disorders associated with expression of PPKH, including gastrointestinal disorders, immune system disorders, neurological disorders and cell proliferative disorders, including cancer.

b
661 GTGATATAAGTGTTCACGACCAAAAAA 707

Sequence 639 Br; 101 R; 430 C; 205 G; 103 T; 0 Other;
 Query Match 99.4%; Score 703; DB 22; Length 839;
 Local Similarity 100.0%; Pred. No: 1.e-137;

EST12
AB30482
AAP30482 standard; cDNA; 839 BP.
X

1 TGACCCGCTGRCCTGTGCCCTTTCAGGGATGGCGTGAGCCCCCAACTCTCCCTG
2

QY	61	GTGCTTCGGCCGGGCTTGCGGACTTGCGCTTCCGGCCACTACCGATTC	PI	Kossida S;
Db	134	GTGCTTCGGCCGGGCTTGCGGACTTGCGCTTCCGGCCACTACCGATTC	DR	XX
QY	121	CTGTTGACCTGGGGCTGGGACTCTGTTGTCCTGAGGGAGGGGGCTC	PT	New human tyrosine phosphatase-like enzyme polypeptide, regulators of
Db	194	CTGTTGACCTGGGGCTGGGACTCTGTTGTCCTGAGGGAGGGGGCTC	PT	which are useful for preventing, treating diabetes, obesity, cancer,
QY	181	GACAGCTGCCGGGCTCACCTTGACCGCTTGCGCATCCGCACTTG	PT	cardiovascular and pulmonary diseases -
Db	254	GACAGCTGCCGGGCTCACCTTGACCGCTTGCGCATCCGCACTTG	PT	polynucleotides are useful for screening for modulators which are used
QY	241	CCGACCAAGATGCCCTCTGGAGATGAGGAGGGAGGGAGGGCT	PT	for treating a tyrosine phosphatase-like enzyme dysfunction related
Db	314	CCGACCAAGATGCCCTCTGGAGATGAGGAGGGAGGGAGGGCT	PT	disease such as a central nervous system (CNS) disorder, diabetes,
QY	301	CTGGGACTGACATGTCCTGGGCTTGCCGACTTGACGAGGCCAAC	PT	obesity, chronic obstructive pulmonary disease, cardiovascular disease,
Db	374	CTGGGACTGACATGTCCTGGGCTTGCCGACTTGACGAGGCCAAC	PT	cancer, anorexia, cachexia, wasting disorders, appetite suppression, and
QY	361	GTGAASGAGCAGGGCTTGCTGAGATGCAATTCCGAGACTACGACC	PT	other eating disorder such as bulimia. CNS disorders include brain
Db	434	GTGAGGGCGGGCTTGCTGAGATGCAATTCCGAGACTACGACC	PT	injuries, Parkinson's disease, stroke, multiple sclerosis, Pick's disease,
QY	421	GGCTCATGAGACATGAGGAGGAGAACGACTCTCACAGTCTACAGG	PT	Alzheimer's disease, Huntington's disease, schizophrenia, Creutzfeldt-Jacob dementia, progressive nuclear palsy, and human
Db	494	GGCTCATGAGACATGAGGAGGAGAACGACTCTCACAGTCTACAGG	PT	immunodeficiency virus (HIV) dementia, pain associated with CNS disorders
QY	481	TAGGGCCTTAGTACCCCTACAGGCCCTACCTCCCTCCATGTTGATGG	PT	and cardiovascular diseases include myocardial infarction, ischaemic
Db	554	TAGGGCCTTAGTACCCCTACAGGCCCTACCTCCCTCCATGTTGATGG	PT	diseases of the heart, atrial and ventricular arrhythmia, hypertensive
QY	541	GCCAGAGATGAGGAGTGGACTTAAGTAAACCCCTAGSTCCCATGGCTGAA	CC	vascular diseases and peripheral vascular diseases. The enzyme is useful
Db	614	GCCAGAGATGAGGAGTGGACTTAAGTAAACCCCTAGSTCCCATGGCTGAA	CC	in diagnostic assays for detecting diseases and abnormalities or
QY	601	CACTGAATGAGCCACCCCTGGAGGAGGGCTGATGAGGGAGGGCTGACTGCTT	CC	susceptibility to diseases or abnormalities related to the presence of
Db	674	CACTGAATGAGCCACCCCTGGAGGAGGGCTGACTGCTT 733	CC	mutations in the encoding nucleic acid sequences. The present sequence
QY	661	GTGATAATAGATGTTTACGAAACAAAAAAA 703	CC	represents a human tyrosine phosphatase-like enzyme related DNA.
Db	734	GTGAAATATGAGTTTACGAAACAAAAAAA 776	XX	
SQ Sequence 746 BP; 178 A; 221 C; 218 G; 129 T; 0 other;				
Query Match 95.3%; Score 673.6; DB 24; Length 746;				
Best Local Similarity 99.4%; Preq. No. 1.8e-131; Matches 676; Conservativeness 0; Mismatches 4; Indels 0; Gaps 0;				
Matches 676; Conservativeness 0; Mismatches 4; Indels 0; Gaps 0;				
QY	28	GCGATGGGGCGACGCCCAACTCTCTGGCTCCGGCTGGGGAGCT	QY	28 GCGATGGGGCGACGCCCAACTCTCTGGCTCCGGCTGGGGAGCT
Db	32	GCGATGGGGCGACGCCCAACTCTCTGGCTCCGGCTGGGGAGCT	Db	32 GCGATGGGGCGACGCCCAACTCTCTGGCTCCGGCTGGGGAGCT
QY	88	GCGTGCACGGCTTCCGGCCACTAACCTACAGTGTGTTGACCTG	QY	88 GCGTGCACGGCTTCCGGCCACTAACCTACAGTGTGTTGACCTG
Db	92	GCGTGCACGGCTTCCGGCCACTAACCTACAGTGTGTTGACCTG	Db	92 GCGTGCACGGCTTCCGGCCACTAACCTACAGTGTGTTGACCTG
QY	148	GCTCTCTGACGGGGGGCCCCCTACAGGACGTGCCCCGGCTCACCTGCAC	QY	148 GCTCTCTGACGGGGGGCCCCCTACAGGACGTGCCCCGGCTCACCTGCAC
Db	152	CCCTGGCCATCCCCGACTCTCCCGCCGCCCCCTACAGGACGTGCCCCGGCTCACCTGCAC	Db	152 CCCTGGCCATCCCCGACTCTCCCGCCGCCCCCTACAGGACGTGCCCCGGCTCACCTGCAC
QY	208	CCCTGGCCATCCCCGACTCTCCCGCCGCCCCCTACAGGACGTGCCCCGGCTCACCTGCAC	QY	208 CCCTGGCCATCCCCGACTCTCCCGCCGCCCCCTACAGGACGTGCCCCGGCTCACCTGCAC
Db	212	CCCTGGCCATCCCCGACTCTCCCGCCGCCCCCTACAGGACGTGCCCCGGCTCACCTGCAC	Db	212 CCCTGGCCATCCCCGACTCTCCCGCCGCCCCCTACAGGACGTGCCCCGGCTCACCTGCAC
QY	268	ATCGTGGACGAGGCCAACGACGGGGAGGGCTGGCTGAGTCACGTGTCCTCGGGCT	QY	268 ATCGTGGACGAGGCCAACGACGGGGAGGGCTGGCTGAGTCACGTGTCCTCGGGCT
Db	272	ATCGTGGACGAGGCCAACGACGGGGAGGGCTGGCTGAGTCACGTGTCCTCGGGCT	Db	272 ATCGTGGACGAGGCCAACGACGGGGAGGGCTGGCTGAGTCACGTGTCCTCGGGCT
QY	328	GCGGCACTGGGACCATCTGGCTGTACCTGGCTGAGGAGGGGGCTGGCTGAGA	QY	328 GCGGCACTGGGACCATCTGGCTGTACCTGGCTGAGGAGGGGGCTGGCTGAGA
Db	332	GCGGCACTGGGACCATCTGGCTGTACCTGGCTGAGGAGGGGGCTGGCTGAGA	Db	332 GCGGCACTGGGACCATCTGGCTGTACCTGGCTGAGGAGGGGGCTGGCTGAGA
QY	388	GATGCCAATGCGAATCCGAGACTAGACCCGGCTCATGGACCTATGACAGG	QY	388 GATGCCAATGCGAATCCGAGACTAGACCCGGCTCATGGACCTATGACAGG
Db	392	GATGCCAATGCGAATCCGAGACTAGACCCGGCTCATGGACCTATGACAGG	Db	392 GATGCCAATGCGAATCCGAGACTAGACCCGGCTCATGGACCTATGACAGG
QY	448	AAGCAGCTTCAGTCTACCGAGGAGAAATAGGGCCCTAGTACCTCTTAC	QY	448 AAGCAGCTTCAGTCTACCGAGGAGAAATAGGGCCCTAGTACCTCTTAC
Db	452	AAGCAGCTTCAGTCTACCGAGGAGAAATAGGGCCCTAGTACCTCTTAC	Db	452 AAGCAGCTTCAGTCTACCGAGGAGAAATAGGGCCCTAGTACCTCTTAC
PR	11-SEP-2000; 2000US-231568P.		PR	11-SEP-2000; 2000US-231568P.
XX	06-DEC-2000; 2000US-251403P.		XX	06-DEC-2000; 2000US-251403P.
XX	(FABR) BAYER AG.		XX	(FABR) BAYER AG.

QY	568	GATTAACCTCTAGCTCCATTGCTGAGACATGAACTGAGTASGCCACCCCTCAGGA	627	SQ Sequence 746 BP; 178 A; 221 C; 218 G; 129 T; 0 other;
Db	572	GTTTAAACCTCTAGCTCCATTGCTGAGACATGAACTGAGTASGCCACCCCTCAGGA	631	Query Match 95.3%; Score 673.6; DB 24; Length 746; Best Local Similarity 99.4%; Pred. No. 1.8e-131; Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	628	GGTCTGTGATGAGGGAGGCTTGACTGCTTGTGATAAATGAGTTACGACCA	687	Db 632 GGTCGAGATGAGGGAGGCTTGACTGCTTGTGATAAATGAGTTACGACCA 691
QY	688	AAAAAAAAAAAAAAA 707	711	Db 692 GGAaaaaaaaaaaaaaa 711
Db	692	GGAAAAAA 711		
RESULT 4				
ABL40815				
ID	ABL40815	standard; cDNA; 746 BP.		
XX				
AC	ABL40815;			
XX				
DT	03-JUL-2002	(first entry)		
XX				
DE	Human tyrosine phosphatase-like enzyme encoding cDNA.			
XX				
KW	Tyrosine phosphatase-like enzyme; antidiabetic; anorectic; cytosatic; cardiant; metabolic; immunomodulator; antiparkinsonian; anticonvulsant; cerebroprotective; neuroprotective; nootropic; neuroleptic; anti-HIV; antiarrhythmic; hypotensive; vulnerable; gene therapy; human; gene; ss.			
OS	Homo sapiens.			
XX				
PN	WO200220747-A2.			
XX				
PD	14-MAR-2002.			
XX				
PF	05-SEP-2001; 2001W0-EP10205.			
XX				
PR	11-SEP-2000; 2000US-231568P.			
XX				
PR	06-DEC-2000; 2000US-251403P.			
PA	(FARB) BAYER AG.			
XX				
PT	Kossida S;			
XX				
DR	WPI; 2002-339803/37.			
XX				
PT	New human tyrosine phosphatase-like enzyme polypeptide, regulators of which are useful for preventing, treating diabetes, obesity, cancer, cardiovascular and pulmonary diseases			
XX				
PS	Claim 19; Page 117; 117pp; English.			
XX				
CC	The invention relates to a purified human tyrosine phosphatase-like enzyme polypeptide. The enzyme can be expressed by standard recombinant methodology. The tyrosine phosphatase-like enzyme and encoding polynucleotides are useful for screening for modulators which are used for treating a tyrosine phosphatase-like enzyme dysfunction related disease such as a central nervous system (CNS) disorder, diabetes, obesity, chronic obstructive pulmonary disease, cardiovascular disease, and other eating disorder such as bulimia. CNS disorders include brain injuries, Parkinson's disease, dementia, multiple sclerosis, stroke, Alzheimer's disease, Huntington's disease, schizophrenia, Pick's disease, Creutzfeldt-Jacob dementia, progressive nuclear palsy, and human immunodeficiency virus (HIV) dementia, pain associated with CNS disorders and cardiovascular diseases include myocardial infarction, ischaemic diseases of the heart, atrial and ventricular arrhythmia, hypertensive vascular diseases and peripheral vascular diseases. The enzyme is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of mutations in the encoding nucleic acid sequences. The present sequence represents the human tyrosine phosphatase-like enzyme polypeptide encoding cDNA.			
XX				
RESULT 5				
ABL40807				
ID	ABL40807	standard; DNA; 709 BP.		
XX				
AC	ABL40807;			
XX				
DT	03-JUL-2002	(first entry)		
XX				
DE	Human tyrosine phosphatase-like enzyme related EST sequence #1.			
XX				
KW	Tyrosine phosphatase-like enzyme; antidiabetic; anorectic; cytosatic; cardiant; metabolic; immunomodulator; antiparkinsonian; anticonvulsant; cerebroprotective; neuroprotective; nootropic; neuroleptic; anti-HIV; antiarrhythmic; hypotensive; vulnerable; gene therapy; human; gene; expressed sequence tag; EST; ds.			
XX				
OS	Homo sapiens.			
XX				

PN	WO200220747-12.
PD	14-MAR-2002.
XX	
PF	05-SEP-2001; 2001WO-EP10205.
XX	
PR	11-SEP-2000; 2000US-231568P.
XX	
PR	06-DEC-2000; 2000US-251403P.
XX	
PA	(FRBB) BAYER AG.
XX	
PI	Kossida S;
XX	
DR	WPI; 2002-339803/37.
XX	
PT	New human tyrosine phosphatase-like enzyme polypeptide, regulators of which are useful for preventing, treating diabetes, obesity, cancer, cardiovascular and pulmonary diseases
XX	
PS	Disclosure; Fig 4; 11pp; English.
XX	
CC	The invention relates to a purified human tyrosine phosphatase-like enzyme polypeptide. The enzyme can be expressed by standard recombinant methodology. The tyrosine phosphatase-like enzyme and encoding polynucleotides are useful for screening for modulators which are used for treating a tyrosine phosphatase-like enzyme dysfunction related disease such as a central nervous system (CNS) disorder, diabetes, obesity, chronic obstructive pulmonary disease, cardiovascular disease, cancer, anorexia, cachexia, wasting disorders, appetite suppression, and other eating disorders such as bulimia. CNS disorders include brain injuries, Parkinson's disease, dementia, multiple sclerosis, stroke, Alzheimer's disease, Huntington's disease, schizophrenia, Pick's disease, Creutzfeld-Jacob dementia, progressive nuclear palsy, and human immunodeficiency virus (HIV) dementia, pain associated with CNS disorders and cardiovascular diseases include myocardial infarction, ischaemic diseases of the heart, atrial and ventricular arrhythmia, hypertensive vascular diseases and peripheral vascular diseases. The enzyme is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of mutations in the encoding nucleic acid sequences. Sequences ABL40807-813 represent human tyrosine phosphatase-like enzyme related expressed EST sequence tag (EST) fragments.
XX	
SQ	Sequence 709 BP; 137 A; 233 C; 206 G; 133 T; 0 other:
Query Match	95.0%; Score 671.6; DB 24; Length 709;
Best Local Similarity	98.6%; Pred. No. 4.7e-131;
Matches	688; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Oy	1 TGACCGCTGCTCTGCCCTTCCCCAGCATGGCTGCAGCCCCCACTCTCTGG 60
Db	13 TGACCCGCTGTCCTGCCCTTCCAGCGATGGCTGAGCCCCCACTCTCTGG 72
Oy	61 GTGCTCCGGCGGCGACTGGCGCTGCCAGGGCTCCCGCCCTACCGTT 120
Db	73 GTGCTCCGGCGGCGACTGGCGCTGCCAGGGCTCCCGCCCTACCGTT 132
Oy	121 CTGTTGACCTGGCGGCGACCTGGCTGCCAGGAGCGCGGCCCTCACAGC 180
Db	133 CTGTTGACCTGGCGGCGACCTGGCTGCCAGGAGCGCGGCCCTCACAGC 192
Oy	181 GACAGCTGCCCGGCTTACCCGTGACATCGTGGAGGAGCCAAAGGCCGGAGGT 240
Db	193 GACAGCTGCCCGGCTTACCCGTGACATCGTGGAGGAGCCAAAGGCCGGAGGT 252
Oy	241 CCCGACCATGACGCCCTGGTGTGACATCGTGGAGGAGCCAAAGGCCGGAGGT 300
Db	253 CCCGACCATGACGCCCTGGTGTGACATCGTGGAGGAGCCAAAGGCCGGAGGT 312
Oy	301 GTGGGAGTGAACCTGGCTCTGGCTTGCGCGACTGGCCATCCGACTCTGCCGCC 360
Db	313 GTGGGAGTGAACCTGGCTCTGGCTTGCGCGACTGGCCATCCGACTCTGCCGCC 372
XX	
QY	361 GTGAGGAGCGGGGCTTGGCTGAGGAGATGCCATTGCTGAAATCCGAGACTACGACCC 420
Db	373 GTGAGGAGCGGGGCTTGGCTGAGGAGATGCCATTGCTGAAATCCGAGACTACGACCC 432
QY	421 GGCCCATGAGACCTATGAGCAGGAGAAAGCTTCCAGTCTTACAGCGAACGAA 480
Db	433 GGCCATGAGACCTATGAGCAGGAGAAAGCTTCCAGTCTTACAGCGAACGAA 492
QY	481 TAAGGGCCTAGTACCTCTACCCAGGCCCTACCTCCCTTCCCAGTGTGAGGG 540
Db	493 TAGGGCCCTAGTACCTCTACCCAGGCCCTACCTCCCTTCCCAGTGTGAGGG 552
QY	541 GCCAGAGATGAGGGAAAGTGGACTAAGTAACTCTAGTCCATGGCTGAGA 600
Db	553 GCCAGAGATGAGGGAAAGTGGACTAAGTAACTCTAGTCCATGGCTGAGA 612
QY	601 CACTGAGTAGGCCACCCCTGGAGGAGCTGTGATGAGGGAGSCTGTACTGCTT 660
Db	613 CACTGAGTAGGCCACCCCTGGAGGAGCTGTGATGAGGGAGSCTGTACTGCTT 671
QY	661 GTGATAATGAGTGTACGAAACAAAAAAA 698
Db	672 GTGATAATGAGTGTACGAAACAGGAAAAA 709
XX	
RESULT	6
AR63583	ID AR63583 standard; cDNA; 694 BP.
XX	
AC	AR63583;
XX	
DT	11-MAY-2001 (first entry)
XX	
DE	Human phosphatase BAK91172_h coding sequence.
XX	
KW	phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia; cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia; congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease; Moebius syndrome; Bjornstad syndrome; Bannayan-Zonana syndrome; schizophrenia; hamartoma; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200112819-A2.
XX	
PD	22-FEB-2001.
XX	
PF	11-AUG-2000; 2000WO-US22158.
XX	
PR	13-AUG-1999; 990US-0149005.
XX	
PA	(SUGE-) SUGEN INC.
XX	
PI	Piowlman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;
XX	
DR	WPI; 2001-211226/21.
DR	P-PSDB; AAB73231.
XX	
PT	New protein phosphatase polypeptide for diagnosing and treating PT phosphatase related disorders such as cancer, schizophrenia, cardiac dysfunction and/or vascular disorders
XX	
PS	Claim 1; Fig 4; 138pp; English.
XX	
CC	The present invention relates to phosphatase proteins and coding CC sequences. The present sequence is one such phosphatase coding sequence. CC phosphatases are enzymes that catalyse the dephosphorylation of proteins CC modified by phosphorylation of serine, threonine or tyrosine residues. CC The phosphatases are useful for treating a variety of diseases; for example cancer e.g. breast, urogenital, prostate, head, neck, lung CC cancers, synovial sarcomas, renal cell carcinoma, non-small cell lung CC cancer, hepatocellular carcinoma, pancreatic endocrine tumours, stomach

CC	pathophysiological hypoxia, cardiac dysfunction and/or vascular disorders, myopathies, congenital muscle disorders, papillon-Lefèvre syndrome, Cowden disease, ectodermal dysplasia, Moebius syndrome, Björnstad syndrome, Bannayan-Zonana syndrome, schizophrenia and hamartomas.	OS	Homo sapiens.
CC	sequence 694 BP; 128 A; 221 C; 216 G; 129 T; 0 other;	XX	WO200220747-A2.
CC	Query Match 93.0%; Score 657.4; DB 22; Length 694; Best Local Similarity 99.8%; Pred. No. 4.3e-128; Matches 658; Conservative 0; Mismatches 1; Indels 0; Gaps 0; PR 11-SEP-2000; 2000US-231569P.	XX	PR 06-DEC-2000; 2000US-251403P.
CC	OY 28 GCGATGGCGGCGACGCCCAACTTCTCGTGGCTCCGGCCGGCTGGGGACTG 87 GCGATGGGGTGCAGCCCCCAACTCTCTGTGGCTCCGGCCGGCTGGGGACTG 91	XX	PD 14-MAR-2002.
CC	OY 88 GCGCTGCCGCGACTCCCGCCACTACCTAGGTCTGTGACCTGGGGCACCTG 147 GCGCTGCCGCGACTCCCGCCACTACCTAGGTCTGTGACCTGGGGCACCTG 151	XX	(FARB) BAYER AG.
CC	OY 148 GNGTCCCTGACGGAGCCGGCCCTACAGTCAGCAGCTGGCCGGGACTG 207 GNGTCCCTGACGGAGCCGGCCCTACAGCAGCTGGCCGGGACTG 211	XX	XX
CC	OY 212 GCGCTGCCGATCCCAGTCTGCCCCCTACAGCAGCTGGCCGGGACTG 267 GCGCTGCCGATCCCAGTCTGCCCCCTACAGCAGCTGGCCGGGACTG 271	XX	PT Kossida S;
CC	OY 268 ATCGTGACGAGGCCAACGAGGGAGAGGGCTGGGGACTGCTCGGCTT 327 ATCGTGACGAGGCCAACGAGGGAGAGGGCTGGGGACTGCTCGGCTT 331	XX	PT DR 2002-339803/37.
CC	OY 328 GCGCCGACTGSCACCATGCTSGCCTGTTACCTGGTGAAGGAGGGCTTGCTGAGA 387 GCGCCGACTGSCACCATGCTSGCCTGTTACCTGGTGAAGGAGGGCTTGCTGAGA 391	XX	PS Disclosure: Fig 7; 117pp; English.
CC	OY 388 GATGCCATTGCTGAAATCCGGAGACTAGGACCGGGCCTGAGACCTATGGCAGGG 447 GATGCCATTGCTGAAATCCGGAGACTAGGACCGGGCCTGAGACCTATGGCAGGG 451	XX	The invention relates to a purified human tyrosine phosphatase-like enzyme polypeptide, regulators of cardiovascular and pulmonary diseases -
CC	OY 448 AAAGCAGTCTCAGTCTACCGGAGACGAAATAAGGGCCTAGACCTCTACAGG 507 AAAGCAGTCTCAGTCTACCGGAGACGAAATAAGGGCCTAGACCTCTACAGG 511	CC	which are useful for preventing, treating diabetes, obesity, cancer, other eating disorder such as bulimia. CNS disorders include brain injuries, Parkinson's disease, dementia, multiple sclerosis, Pick's disease, Alzheimer's disease, Huntington's disease, schizophrenia, Creutzfeldt-Jacob dementia, progressive nuclear palsy, and human immunodeficiency virus (HIV) dementia, pain associated with CNS disorders and cardiovascular diseases include myocardial infarction, ischaemic diseases of the heart, atrial and ventricular arrhythmia, hypertensive vascular diseases and peripheral vascular diseases. The enzyme is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of mutations in the encoding nucleic acid sequences. Sequences ABL4007-813 represent human tyrosine phosphatase-like enzyme related expressed sequence tag (EST) fragments.
CC	OY 508 GGCCTCACTCCCTCCACCTGTGGTGAAGGGCCAGAGTGAAGGGAGGACTAA 567 GGCCTCACTCCCTCCACCTGTGGTGAAGGGCCAGAGTGAAGGGAGGACTAA 571	XX	Sequence 602 BP; 109 A; 202 C; 179 G; 110 T; 2 other;
CC	Query Match 82.6%; Score 583.8; DB 24; Length 602; Best Local Similarity 99.3%; Pred. No. 9.5e-113; Matches 596; Conservative 0; Mismatches 3; Indels 1; Gaps 1; PR 05-SEP-2001; 2001WO-EP10205.	XX	PR 06-DEC-2000; 2000US-251403P.
CC	OY 568 GTTAAACCCCTCTASCTCCATGGTGAAGGAGACACTGAGAATGGCCACCCCTGAGCA 627 GTTAAACCCCTCTASCTCCATGGTGAAGGAGACACTGAGAATGGCCACCCCTGAGCA 631	XX	XX
CC	OY 628 GGTCCTGATGAGGGAGGCTGTACTGCTTGTGAATAATGAGTTAGAACCA 686 GGTCCTGATGAGGGAGGCTGTACTGCTTGTGAATAATGAGTTAGAACCA 690	XX	XX
CC	RESULT 7 ABL40810 standard; DNA; 602 BP.	XX	XX
CC	ID ABL40810;	XX	XX
CC	XX Human tyrosine phosphatase-like enzyme related EST sequence #4.	XX	XX
CC	Tyrosine phosphatase-like enzyme; antidiabetic; cyrotactic; cardiotoxic; metabolic; immunomodulator; anti-parkinsonian; anticonvulsant; cerebroprotective; neuroprotective; nootropic; neuroleptic; anti-HIV; antiarrhythmic; hypotensive; vulnerable; gene therapy; human; gene; expressed sequence tag; EST; ds.	XX	XX
CC	xx	xx	xx

Db 303 CATCCTGGCTTACCTGGTAANGGACCGNGNCTTGCTCCAGAGATGCCATTGCG 362
 QY 401 AAATCCGAGCATACGACCGGCAGTCATCGAGACCTATGAGCAGAGAACAGCTTCCC 460
 Db 363 AAATCCGAGCATACGACCGGCAGTCATCGAGACCTATGAGCAGAGAACAGCTTCCC 422
 QY 461 AGTTCTACCGAGAACAAATAGGGCTTACCTTACCAAGGCCACTCCCC 520
 Db 423 AGTTCTACCGAGAACAAATAGGGCTTACCTTACCAAGGCCACTCCCC 482
 QY 521 TTCCCACTGTGATGGGGAGAGATGAAGGAAGTGGACTAAGTAAACCTC 580
 Db 483 TAGTCCCATTGCTGAAAGACTAGAATGGCCACCCCTGAGGAGTCAGTCAA 542
 QY 581 TAGTCCCATTGCTGAAAGACTAGAATGGCCACCCCTGAGGAGTCAGTCAA 640
 Db 543 TAGTCCCATTGCTGAAAGACTAGAATGGCCACCCCTGAGGAGTCAGTCAA 602

RESULT 8

AB140812
 ID ABL40812 standard; DNA; 553 BP.
 XX AC
 XX AB140812;
 XX DT 03-JUL-2002 (first entry)
 Human tyrosine phosphatase-like enzyme related EST sequence #6.

KW Tyrosine phosphatase-like enzyme; antidiabetic; anorectic; cytostatic; cardiotonic; metabolic; immunomodulator; anti-parkinsonian; anticonvulsant; cerebroprotective; neuroprotective; nootropic; neuroleptic; anti-HIV; antiarrhythmic; hypotensive; vulnerary; gene therapy; human; gene; expressed sequence tag; EST; ds.

OS Homo sapiens.

XX WO200220747-A2.

XX 14-MAR-2002.

XX PF 05-SEP-2001; 2001WO-EP10205.

XX PR 11-SEP-2000; 2000US-231568P.
 06-DEC-2000; 2000US-251403P.

XX PA (FARB) BAYER AG.

XX PT Kossida S;

XX DR WO200220747-A2.

XX PR New human tyrosine phosphatase-like enzyme polypeptide, regulators of protein which are useful for preventing, treating diabetes, obesity, cancer, cardiovascular and pulmonary diseases

PS Disclosure; Fig 9; 117pp; English.

CC The invention relates to a purified human tyrosine phosphatase-like enzyme polypeptide. The enzyme can be expressed by standard recombinant methodology. The tyrosine phosphatase-like enzyme and encoding polynucleotides are useful for screening for modulators which are used for treating a tyrosine phosphatase-like enzyme dysfunction related disease such as a central nervous system (CNS) disorder, diabetes, obesity, chronic obstructive pulmonary disease, cardiovascular disease, cancer, anorexia, cachexia, wasting disorders, appetite suppression, and other eating disorder such as bulimia. CNS disorders include brain injuries, Parkinson's disease, multiple sclerosis, stroke, Alzheimer's disease, Huntington's disease, schizophrenia, Pick's disease, Creutzfeldt-Jacobs dementia, progressive nuclear palsy, and human immunodeficiency virus (HIV) dementia. pain associated with CNS disorders and cardiovascular diseases include myocardial infarction, ischaemic diseases of the heart, atrial and ventricular arrhythmia, hypertensive

OC vascular diseases and peripheral vascular diseases. The enzyme is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of mutations in the encoding nucleic acid sequences. Sequences AB140807-813 represent human tyrosine phosphatase-like enzyme related expressed sequence tag (EST) fragments.

XX Sequence 553 BP; 96 A; 186 C; 168 G; 103 T; 0 other;

XX SQ Best Local Similarity 71.9%; Score 508.6; DB 24; Length 553; Matches 545; Conservative 0; Mismatches 4; Indels 4; Gaps 3;

Query Match 71.9%; Score 508.6; DB 24; Length 553; Best Local Similarity 98.6%; Pred. No. 4.6e-97; Matches 545; Conservative 0; Mismatches 4; Indels 4; Gaps 3;

QY 29 CGATGGGAGTGACGCCAACATCTCTGGGCTTGGGGAGCCGCTGGGGACCTGG 88
 Db 1 CGATGGGAGTGACGCCAACATCTCTGGGCTTGGGAGCTGGCTTGGGGACCTGG 60

QY 89 CGCUCCCCGGCCCGCCCGCCACTTACCGATCTGGTGACCGCCGGCTGGCGACCTGG 148
 Db 61 CGCUCCCCGGCCCGCCCGCCACTTACCGATCTGGTGACCGCCGGCTGGCGACCTGG 120

QY 149 TGCCTCTACG - SGAGCCGGGCCCTCACAGGACCTGCCCCGGCTAACCTCGCA 206
 Db 181 CGCCTGGCATCCCTGACTCTGCGCCGGCCCGCACCGACGCTGGGAGTGACTGTCGTC 180

QY 266 AGATGTGAGTGGCTGACGTCAGTCGGACGGAGGGAGCTGTTGGAGTGACTGTCGTC 265
 Db 241 AGATGTGAGTGGCTGACGTCAGTCGGACGGAGGGAGCTGTTGGAGTGACTGTCGTC 300

QY 325 TTRGCCCACTTGACCATGCGGCTGTACTCTGGAGAGGAGGGCTGGCGCA 384
 Db 301 TTRGCCCACTTGACCATGCGGCTGTACTCTGGAGAGGAGGGCTGGCGCA 360

QY 385 GGAGATGCCATTGCTGAATCCGACGACTACGCCGGCTCATCGAGAACCTATGAGGAG 444
 Db 361 GGAGATGCCATTGCTGAATCCGACGACTACGCCGGCTCATCGAGAACCTATGAGGAG 420

QY 445 GAGAAGAGTCTCCACTCTTACCGAGAACAAATAGGGCTTGTACTCTCTCTAC 504
 Db 421 GAGAAGAGTCTCCACTCTTACCGAGAACAAATAGGGCTTGTACTCTCTAC 480

QY 505 CAGGCCCTCACTCCCTTCCCACTGTCATGGGGCAGAGATGGGGAGTGGACT 564
 Db 481 CAGGCCCTCACTCCCTTCCCACTGTCATGGGGCAGAGATGGGGAGTGGACT 540

QY 555 AAAGTATTAAACC 577
 Db 541 AAAGTATTAAACC 553

RESULT 9

AB140808
 ID ABL40808 standard; DNA; 493 BP.
 XX AC
 XX AB140808;
 XX DT 03-JUL-2002 (first entry)
 Human tyrosine phosphatase-like enzyme related EST sequence #2.

KW Tyrosine phosphatase-like enzyme; antidiabetic; anorectic; cytostatic; cardiotonic; metabolic; immunomodulator; anti-parkinsonian; anticonvulsant; cerebroprotective; neuroprotective; nootropic; neuroleptic; anti-HIV; expressed sequence tag; EST; ds.

OS Homo sapiens.

XX WO200220747-A2.

XX
PD 14-MAR-2002.
XX
PT 05-SEP-2001; 2001WO-EP10205.
XX
PR 11-SEP-2000; 2000US-23158P.
XX
PR 06-DEC-2000; 2000US-251403P.
XX
PA (FARB) BAYER AG.
XX
PI Kossida, S.
XX
DR WPI; 2002-339803/37.
XX
PT New human tyrosine phosphatase-like enzyme polypeptide regulators of PT which are useful for preventing, treating diabetes, obesity, cancer, cardiovascular and pulmonary diseases
XX
PS Disclosure; Fig 5; 117pp; English.
XX
CC The invention relates to a purified human tyrosine phosphatase-like enzyme polypeptide. The enzyme can be expressed by standard recombinant methodology. The tyrosine phosphatase-like enzyme and encoding polynucleotides are useful for screening for modulators which are used for treating a tyrosine phosphatase-like enzyme dysfunction related disease such as a central nervous system (CNS) disorder, diabetes, obesity, chronic obstructive pulmonary disease, cardiovascular disease, cancer, anorexia, cachexia, wasting disorders, appetite suppression, and other eating disorder such as bulimia. CNS disorders include brain injuries, Parkinson's disease, dementia, multiple sclerosis, stroke, Alzheimer's disease, Huntington's disease, schizophrenia, Pick's disease, Creutzfeldt-Jacob dementia, progressive nuclear palsy, and human immunodeficiency virus (HIV) dementia, pain associated with CNS disorders and cardiovascular diseases include myocardial infarction, ischaemic diseases of the heart, atrial and ventricular arrhythmia, hypertension, vascular diseases and peripheral vascular diseases. The enzyme is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of mutations in the encoding nucleic acid sequences. Sequences AB040807-813 represent human tyrosine phosphatase-like enzyme related expressed sequence tag (EST) fragments.
XX
Sequence 493 BP; 78 A; 176 C; 149 G; 90 T; 0 other;
XX
Query Match 68.8%; Score 46.2; DB 24; Length 493;
Best Local Similarity 99.4%; Pred. No. 2.1e-92; PI 0; Mismatches 488; Conservative 0; Indels 3; Gaps 0; Gaps 0;
XX
Qy 42 GCCCCCAACTTCTGCTGGCTCGGGGGCTGGGGACTGGCGTGGGGGT 101
Db 3 GGGCGGCCAACTTCCTCTGGGTGCTCGGGGGCTGGGGACTGGCGTGGGGGT 62
Qy 102 CCCGGCCACTACAGTCTGTTGGACCTGGCTGGCACCTGGTGGTGGACCGA 161
Db 63 CC CGCCGCACTACAGTCTGTTGGACCTGGCTGGCACCTGGTGGACGA 122
Qy 162 GCGGGGGCCCTACASGACASCTGGCCCGSCTCACCTCACCGCTGGCATCC 221
Db 123 GCGGGGGCCCTACAGGCACAGCTGCCCCGGCTCACCTCACCGCTGGCATCC 182
Qy 222 CGACUTCTGCCCGGCCGCCCCGACCAGATCGACCGCTTGTCAGATGTTGGAGGGC 281
Db 183 CGACTCTGCCCGGCCGCCCCGACCAGATCGACCGCTTGTCAGATGTTGGAGGGC 242
Qy 282 CAGGCACGGGAGGGCTGGAAGTGTGACTCTGCTGGCTGGCCGACTGGCAC 341
Db 243 CAGGCACGGGAGGGCTGGAAGTGTGACTCTGCTGGCTGGCCGACTGGCAC 302
Qy 342 CATCTGCTGTTGACTCTGGAGGAGGGCTTGAGGAGGAGGCTGCTGCTGCA 401
Db 303 CATCTGCTGCTGTTGACTCTGGAGGAGGGCTTGAGGAGGAGGCTGCTGCA 362
Qy 402 ARCCGAGGACTGACCCGCTCATGAGACTATGAGGAGGAGGAGGAGGCTGCTCCA 461

RESULT 10
DB ABQ56155
ID ABQ56155 standard; cDNA; 559 BP.
XX
DE Human ovarian antigen HVAJ27 cDNA, SEQ ID NO: 2035.
XX
AC ABQ56155;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HVAJ27 cDNA, SEQ ID NO: 2035.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US18569.
XX
PR 07-JUN-2000; 2000US-209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
XX
PR -PSDB; ABP43078.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g., ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.
XX
PS Claim 1; SEQ ID NO 2035; 2922pp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (AB054131-AB05605), and also encompasses polypeptides 90% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, pronosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

CC blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the invention.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 559 BP; 90 A; 192 C; 169 G; 101 T; 7 other;

SQ Best Local Similarity 99.6%; Score 471.8; DB 24; Length 559;
Matches 473; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 15 GTCGCCCTTCCACAGATGGCGGCGAGCCCCCACTTCTCCCTGGGTCTCCGGCG 74
Db 72 GTCCGCCTTTCAGCAGATGGCGGTCTCCGGCG 131

OY 75 GCTGGGGGACTGGGCTGCCGGCTCCCGCCACTACCACTTCTGTGAACTGG 134
Db 132 GCTGGGGGACTGGGCTGCCGGCTCCCGCCACTACCACTTCTGTGAACTGG 191

OY 135 CGTGGGGCACCTGGTCTCCCTGACGGAGCGGGGCCCTACAGCACAGTGCCCCGG 194
Db 192 CGTGGGGCACCTGGTCTCCCTGACGGAGCGGGGCCCTACAGCACAGTGCCCCGG 251

OY 195 CCTCACCCGACCCSCTSGCATCCGACTTCGCCCCGCGGCCAACAGATCGA 254
Db 252 CCTCACCCGACCCSCTSGCATCCGACTTCGCCCCGCGGCCAACAGATCGA 311

OY 255 CGCCTTGCGCAGATGTCGAGGAGGGCCAGCAGGGAGGGCTGTGGAGTCAG 314
Db 312 CGCCTTGCGCAGATGTCGAGGAGGGAGGGCTGTGGAGTCAG 371

OY 315 TGCCTCTGGGTITGGCGACTGGCACCATCTGGCTTACCTGGTGAAGGAGGGGG 374
Db 372 TGCCTCTGGGTITGGCGACTGGCACCATCTGGCTTACCTGGTGAAGGAGGGGG 431

OY 375 CTGCTGTCGAGGAGGAGTGTGCAATTGCGAAATTCGGAGACTAGACCGGGCICATGAGAC 434
Db 432 CTGCTGTCGAGGAGGAGTGTGCAATTGCGAAATTCGGAGACTAGACCGGGCICATGAGAC 491

OY 435 CTATGAGCAGGAGAAAGCAGTCTCCAGTTACAGCGAAATAAGGGCC 489
Db 492 CTATGAGCAGGAGAAAGCAGTCTCCAGTTACAGCGAAATAAGGGCC 546

RESULT 11

ABL0813/C Query Match XX
ID ABL0813 standard; DNA; 448 BP. PD 14-MAR-2002.
XX DE Human tyrosine phosphatase-like enzyme related EST sequence #7. PR 05-SEP-2001; 2001WO-EPI0205.
XX

Tyrosine phosphatase-like enzyme; antidiabetic; anorectic; cytostatic; cardiotonic; metabolic; immunomodulator; antiparkinsonian; anticonvulsant; cerebroprotective; neuroprotective; nootropic; neuroleptic; anti-HIV; antiarrhythmic; hypotensive; vulnerary; gene therapy; human; gene; expressed sequence tag; EST; ds.

XX Homo sapiens.

OS WO200220747-A2.

SQ Sequence 448 BP; 93 A; 132 C; 120 G; 103 T; 0 other;

OY Best Local Similarity 100.0%; Score 446; DB 24; Length 448;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 CCCGACCAAGATGACCGCTCTGTGAGATGCTGGAGGAGCGGCCAGCAAGGGAGAGCT 300
Db 448 CCCGACCAAGATGACCGCTCTGTGAGATGCTGGAGGAGCGGCCAGCAAGGGAGAGCT 389

OY 301 GTGGGAGTGCAGTGTGCTCTGGCTTGGCCACTGGCACCATGCTGGCTGTGTACCTG 360
Db 388 GTGGGAGTGCAGTGTGCTCTGGCTTGGCCACTGGCACCATGCTGGCTGTGTACCTG 329

OY 361 GTGAAGGAGGGGGCTTGGCTGAGGAGATGCCATGCTGAATCGGACACTAGACCC 420
Db 328 GTGAAGGAGGGGGCTTGGCTGAGGAGATGCCATGCTGAATCGGACACTAGACCC 269

OY 421 GGCTCCATTCGAGACCTATGAGCAGGAAGAAGCAGTCTCCAGTCTACCGAGAACGAA 480
Db 268 GGCTCCATTCGAGACCTATGAGCAGGAAGAAGCAGTCTCCAGTCTACCGAGAACGAA 209

OY 481 TAAGGGCTTAGTACCTCTACAGGCCCTACTCCCCTCCCACTGTGTGCTGATGG 540
Db 208 TAAGGGCTTAGTACCTCTACAGGCCCTACTCCCCTCCCACTGTGTGCTGATGG 149

OY 541 GCCAGAGATAAGGAAGTAGCTAAAGTAACCCCTAGCPOCCATGGCTGACA 600
Db 148 GCCAGAGATAAGGAAGTAGCTAAAGTAACCCCTAGCPOCCATGGCTGACA 89

OY 601 CACTGAGTAGCCCCACCCCTGCAGGCGAGGCTCTGATTAACCCCTAGCPOCCATGGCTGACA 660

QY 265 CAGATGTTGGAGCAGGCCAACGCCACGGGAGGGCTGGAGTGACTGTGTCGGGC 324
Db 254 CAGATGTTGGAGCAGGCCAACGCCACGGGAGGGCTGGAGTGACTGTGTCGGGC 313
QY 325 TTGCGCGCACTTGGCACCATGCTGCTGTAACCTGTGAAGGACGGGCTTGGCTGCA 384
Db 314 TTGGCGCACTTGGCACCATGCTGCTGCTGTAACCTGTGAAGGACGGGCTTGGCTGCA 373
QY 385 GGAGATGCCAATGCTGAAATCCG 407
Db 374 GGAGATGCCAATGCTGAAATCCG 396

RESULT 15
AAF27959
ID AAF27959 standard; DNA; 453 BP.
XX
AC AAF27959;
XX
DT 08-MAY-2001 (first entry)
DE Murine dual specificity phosphatase DSP-11 coding sequence.
XX
KW Mouse; dual specificity phosphatase; DSP-11; Duchenne muscular dystrophy;
KW MAP kinase signalling cascade; cell proliferation; cancer; allergy; graft-versus-host disease; autoimmune disease; metabolic disease; ss.
XX
OS Mus sp.
XX
PN WO200105983-A1.
XX
PD 25-JAN-2001.
XX
PR 19-JUL-2000; 2000WO-US19710.
XX
PR 20-JUL-1999; 99US-0144557.
XX
PA (CEPT-) CEPTYR INC.
XX
PI Luche RM, Wei B;
XX
WPI; 2001-147348/15.
XX
DR P-PSDB; AAB35276.
XX
PT Novel dual specificity phosphatase-11 dephosphorylating activated
PT mitogen-activated protein kinase, is used to identify agents inhibiting
PT the enzyme activity and modulate cell proliferation
XX
PS Example 3; Fig 5; 65pp; English.

The present invention provides the protein and coding sequences of the human dual-specificity phosphatase DSP-11. The protein is involved in the MAP-kinase signalling cascade. The sequences can be used in the diagnosis and treatment of Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth and abnormal cell proliferation. The present sequence is the mouse DSP-11 coding sequence.

Sequence 453 BP; 82 A; 144 C; 141 G; 86 T; 0 other;

Query Match 52.8%; Score 373; DB 22; Length 453;
Best Local Similarity 89.0%; Pred. No. 8.8e-69;
Matches 403; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 31 ATGGCGCGAGCCGCCAACCTCTGCTGGTCTGGACCTGGGCTGGGGACTGGG 90
Db 1 ATGGCGCGAGCCGCCAACCTCTGCTGGTCTGGACCTGGGCTGGGGACTGGG 60
QY 91 CTGGCGCGAGCCGCCAACCTCTGCTGGTCTGGACCTGGGCTGGGGACTGGG 150
Db 61 TTGGCGCGAGCCGCCAACCTCTGCTGGTCTGGACCTGGGCTGGGGACTGGG 120
QY 151 TCCCTGACGGAGGGGGCTCACAGCGCACAGTGCCCCCTCACCTGACCGC 210

Db 121 TCCCTGACGGAGGGGGCACCCCTACAGTGACAGCTGTCCGGGCTCACGGCA 180
QY 211 CTGGCGATCCCGACTCTGSCCGGGGGCCGAGGCTGGCTGCGCTTGCGAGTC 270
Db 181 ATGGCGATCCCGACTCTGSCCGGGCCGAGGCTGGCTGCGCTTGCGAGTC 240
QY 271 GTGGACGAGGCCAACCCACGGGAGGCTGGGACTGACTGCTCTGGCTTGCG 330
Db 241 GTGGACGAGGCCAACCCACGGGAGGCTGGGACTGACTGCTCTGGCTTGCG 300
QY 331 CGCACTGGCACCATGCTGCTGTGACCTGGTGAAGGAGGGGGCTTGCGTAGGAGAT 390
Db 301 CGACATGGCACATGCTGCTGTGACTTGCGAGGAGGGCTTGCGCCAGAGAT 360
QY 391 GCATATGCTGAATCCGAGACTAGCACCCTGCATCGACCTATGAGCAGGAAA 450
Db 361 GCCATATGCTGAGATCGGGCGCTGCACAGATGAGCTGAGGAGAAG 420
QY 451 GCAGCTTCCAGTTCTACACGGGACGAATAA 483
Db 421 GCGCTCTCCAGTTCTACACGGGACAAATGA 453

Search completed: November 4, 2002, 08:02:41
Job time : 262 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2002, 08:49:32 ; Search time 48 Seconds
(without alignments)
4907.093 Million cell updates/sec

Title: US-09-619-380-1

Perfect score: 707

Sequence: 1 tgaccgcgtgtccgtgcc...aaaaaaa...aaaaaaaaaaaaaa 707

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 310279 seqs, 166577418 residues

Total number of hits satisfying chosen parameters: 620558

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	241.8	34.2	247	10 US-09-619-824A-73	Sequence 73, Appl
c 2	241.8	34.2	119	10 US-09-747-835A-11	Sequence 11, Appl
c 3	49.2	7.0	1467	10 US-09-747-835A-14	Sequence 14, Appl
c 4	49.2	7.0	2936	10 US-09-747-835A-12	Sequence 12, Appl
c 5	4.5	6.4	3721	12 US-09-030-342-34	Sequence 34, Appl
c 6	44.6	6.3	1366	10 US-09-917-800A-1527	Sequence 1527, Appl
c 7	44.6	6.3	2455	10 US-09-917-800A-1386	Sequence 1386, Appl
c 8	6.3	6.3	1680	10 US-09-815-242-798	Sequence 798, Appl
c 9	43.8	6.2	1815	10 US-09-758-269-13	Sequence 13, Appl
c 10	43.6	6.2	4282	10 US-09-771-927A-12	Sequence 16, Appl
c 11	43.6	6.2	4366	12 US-09-044-666-16	Sequence 666, Appl
c 12	42.8	6.1	6000	10 US-09-764-860-768	Sequence 768, Appl
c 13	42.2	6.0	391	10 US-09-747-835A-10	Sequence 10, Appl
c 14	42.2	6.0	1347	10 US-09-815-242-792	Sequence 792, Appl
c 15	42	5.9	298	10 US-09-759-143-399	Sequence 399, Appl
c 16	42	5.9	298	10 US-09-780-669-399	Sequence 399, Appl
c 17	42	5.9	298	10 US-09-822-827-399	Sequence 399, Appl
c 18	42	5.9	550	10 US-09-925-301-677	Sequence 677, Appl
c 19	5.9	2419	10 US-09-939-408A-12	Sequence 12, Appl	

ALIGNMENTS

RESULT 1	US-09-619-824A-73/C	Sequence 73, Application US/0964824A	Patient No. US/2020102531A1
; GENERAL INFORMATION:			
; APPLICANT: Holtzman, Stephen			
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sigr			
; FILE REFERENCE: 689240-73			
; CURRENT APPLICATION NUMBER: US/09/964,824A			
; CURRENT FILING DATE: 2001-09-27			
; PRIORITY APPLICATION NUMBER: US/60/236,033			
; PRIORITY FILING DATE: 2000-03-28			
; PRIORITY APPLICATION NUMBER: US/60/236,032			
; PRIORITY FILING DATE: 2000-03-28			
; NUMBER OF SEQ ID NOS: 583			
; SOFTWARE: Patentin version 3.0			
; SEQ ID NO: 73			
; LENGTH: 247			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; US-09-964-824A-73			
; Query Match			
; Best Local Similarity 34.2%; Score 241.8; DB 10; Length 247;			
; Matches 243; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
; Sequence 1, Appl			
; Sequence 12, Appl			
; Sequence 34, Appl			
; Sequence 1527, Appl			
; Sequence 73, Appl			
; Sequence 11, Appl			
; Sequence 14, Appl			
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Sequence 71, Appl
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Sequence 91, Appl
Sequence 101, Appl
Sequence 111, Appl
Sequence 121, Appl
Sequence 131, Appl
Sequence 141, Appl
Sequence 151, Appl
Sequence 161, Appl
Sequence 171, Appl
Sequence 181, Appl
Sequence 191, Appl
Sequence 201, Appl
Sequence 211, Appl
Sequence 221, Appl
Sequence 231, Appl
Sequence 241, Appl
Sequence 251, Appl
Sequence 261, Appl
Sequence 271, Appl
Sequence 281, Appl
Sequence 291, Appl
Sequence 301, Appl
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Sequence 321, Appl
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Sequence 361, Appl
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Sequence 391, Appl
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Sequence 521, Appl
Sequence 531, Appl
Sequence 541, Appl
Sequence 551, Appl
Sequence 561, Appl
Sequence 571, Appl
Sequence 581, Appl
Sequence 591, Appl
Sequence 601, Appl
Sequence 611, Appl
Sequence 621, Appl
Sequence 631, Appl
Sequence 641, Appl
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Sequence 661, Appl
Sequence 671, Appl
Sequence 681, Appl
Sequence 691, Appl
Sequence 701, Appl
Sequence 711, Appl
Sequence 721, Appl
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Sequence 771, Appl
Sequence 781, Appl
Sequence 791, Appl
Sequence 801, Appl
Sequence 811, Appl
Sequence 821, Appl
Sequence 831, Appl
Sequence 841, Appl
Sequence 851, Appl
Sequence 861, Appl
Sequence 871, Appl
Sequence 881, Appl
Sequence 891, Appl
Sequence 901, Appl
Sequence 911, Appl
Sequence 921, Appl
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Sequence 951, Appl
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Sequence 981, Appl
Sequence 991, Appl
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Sequence 1011, Appl
Sequence 1021, Appl
Sequence 1031, Appl
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Sequence 1061, Appl
Sequence 1071, Appl
Sequence 1081, Appl
Sequence 1091, Appl
Sequence 1101, Appl
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Sequence 1121, Appl
Sequence 1131, Appl
Sequence 1141, Appl
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Sequence 1181, Appl
Sequence 1191, Appl
Sequence 1201, Appl
Sequence 1211, Appl
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Sequence 1231, Appl
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Sequence 1311, Appl
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Sequence 1421, Appl
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Sequence 1561, Appl
Sequence 1571, Appl
Sequence 1581, Appl
Sequence 1591, Appl
Sequence 1601, Appl
Sequence 1611, Appl
Sequence 1621, Appl
Sequence 1631, Appl
Sequence 1641, Appl
Sequence 1651, Appl
Sequence 1661, Appl
Sequence 1671, Appl
Sequence 1681, Appl
Sequence 1691, Appl
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Sequence 1711, Appl
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Sequence 1831, Appl
Sequence 1841, Appl
Sequence 1851, Appl
Sequence 1861, Appl
Sequence 1871, Appl
Sequence 1881, Appl
Sequence 1891, Appl
Sequence 1901, Appl
Sequence 1911, Appl
Sequence 1921, Appl
Sequence 1931, Appl
Sequence 1941, Appl
Sequence 1951, Appl
Sequence 1961, Appl
Sequence 1971, Appl
Sequence 1981, Appl
Sequence 1991, Appl
Sequence 2001, Appl
Sequence 2011, Appl
Sequence 2021, Appl
Sequence 2031, Appl
Sequence 2041, Appl
Sequence 2051, Appl
Sequence 2061, Appl
Sequence 2071, Appl
Sequence 2081, Appl
Sequence 2091, Appl
Sequence 2101, Appl
Sequence 2111, Appl
Sequence 2121, Appl
Sequence 2131, Appl
Sequence 2141, Appl
Sequence 2151, Appl
Sequence 2161, Appl
Sequence 2171, Appl
Sequence 2181, Appl
Sequence 2191, Appl
Sequence 2201, Appl
Sequence 2211, Appl
Sequence 2221, Appl
Sequence 2231, Appl
Sequence 22

Sequence 12 Application US-09747835A
 Patent No US2002014659A1
GENERAL INFORMATION:
 APPLICANT: Yamazaki, Victoria
 APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Zhou, Ping
 APPLICANT: Wang, Dunrui
 APPLICANT: Ren, Feiyun
 APPLICANT: Asundi, Vinod
 APPLICANT: Dianmac, Radote T
 TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
 TITLE OF INVENTION: LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
 FILE REFERENCE: HYS-37CIP
 CURRENT APPLICATION NUMBER: US-09/747,835A
 CURRENT FILING DATE: 2002-03-08
 PRIOR APPLICATION NUMBER: US 09/729,739
 PRIOR FILING DATE: 2000-12-04
 PRIOR APPLICATION NUMBER: US 09/653,450
 PRIOR FILING DATE: 2000-08-31
 PRIOR APPLICATION NUMBER: US 09/620,312
 PRIOR FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: US 09/598,042
 PRIOR FILING DATE: 2000-06-20
 PRIOR APPLICATION NUMBER: US 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: US 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID: 63
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 12
 LENGTH: 2936
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (135)..(1601)
 US-09-747-835A-12

Query Match	7.0%	Score	49.2	DB	10	Length	2936
Best Local Similarity	46.7%	Pred.	No. 0.028				
Matches	156;	Conservative	0;	Mismatches	178;	Indels	0;
						Gaps	0;
QY	65	"TCGCCGGCCGCTGGCGGACATGGCGCAGCCGGCCTCCCGCCACTAACAGTCTGT					
QY	949	TGCCCGGGGGCTGCTGGCGCTGGCGCTGGCGCTGGCGACCAAGTACAGCGCTTCC					
QY	125	TGACCTGGCGTGCGCACCTGGTCCCCGACGGAGCCGGCCCTACAGCGACA					
QY	1009	CGACATGGCTGGACACTGGCTACAGCACCGAACAGAGATGGCGCTCTCACTTCCT					
QY	185	GCTGCCGGCCCTACCTGCAACGCCCTGGCGATCCCGGACATTGGCGCTGGCGCTGGCGCCACCG					
QY	1069	GGCCGCCTCTGACGCCCTACAGCTCTGCTGGCGCTGGCGCCACCGCTACG					
QY	245	ACCAGATCGAACGGCTCTGGCAGATCTGGAGGAGCCACCGGGAGGGCTGG					
QY	1119						
QY	1129	ACCTGGTCACCTGGCAGTCAGCAGGCTCTGGCCAAACAGAGCCACCTCTGGTGGAGG					
QY	305	GAGTGCCTGCTCTGGCTTGCCGACCTGGCACCATGGTGGCTGTACTTGGTGA					
QY	365	AGGAGCGGGCTTGCGCTGAGGAGATGGCTGGAGTCCTGGCCCTCGGCACCGTGT					
QY	1249	CCCTGCTGGCGCTGACCTCACTGGCGTCCATGG					

304
 1188
 398
 1248

RESULTS
US-10-036-342-34
; Sequence 34, Application US/10036342
; Patent No. US20020090681A1

PRIOR FILING DATE: 1999-08-25
 PRIOR APPLICATION NUMBER: 09/644848
 PRIOR FILING DATE: 2000-08-22
 PRIOR APPLICATION NUMBER: 09/747259
 PRIOR FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: 09/816744
 PRIOR FILING DATE: 2001-03-22
 PRIOR APPLICATION NUMBER: 09/854208
 PRIOR APPLICATION NUMBER: 09/854280
 PRIOR FILING DATE: 2001-05-10
 PRIOR APPLICATION NUMBER: 09/874503
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: 09/869599
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: 09/908,827
 PRIOR FILING DATE: 2001-07-18
 PRIOR APPLICATION NUMBER: PCT/US99/10733
 PRIOR FILING DATE: 1999-05-14
 PRIOR APPLICATION NUMBER: PCT/US99/28551
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/30720
 PRIOR FILING DATE: 1999-12-22
 PRIOR APPLICATION NUMBER: PCT/US00/05601
 PRIOR FILING DATE: 2000-03-01
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: 2000-05-22
 PRIOR APPLICATION NUMBER: PCT/US00/15264
 PRIOR FILING DATE: 2000-06-02
 PRIOR APPLICATION NUMBER: PCT/US00/23522
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: PCT/US00/23328
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: 2000-12-01
 PRIOR APPLICATION NUMBER: PCT/US00/34956
 PRIOR FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: PCT/US01/17800
 PRIOR FILING DATE: 2001-06-01
 PRIOR APPLICATION NUMBER: PCT/US01/19692
 PRIOR FILING DATE: 2001-06-20
 PRIOR APPLICATION NUMBER: PCT/US01/21066
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: PCT/US01/21735
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 80
 SEQ ID NO 34
 LENGTH: 3721
 TYPE: DNA
 ORGANISM: Homo Sapien
 -10-036-342-34

Query Match 6.4%; Score 45; DB 12; Length 3721;
 Best Local Similarity 49.0%; Pred. No. 0.26; Mismatches 120; Conservative 0; Indels 0; Gaps 0;

39 GGAGCCCCCAACTCTCTGGGTGCTCCGGCCGGACTGGCGTGGCGG 98
 2187 GGACCCGACCCACGGCCCTGGCCGCCGCGCTGGCGGACCGAGCCACCCCTGGCGC 2246
 99 GCGCCGCCACTACAGTTCTGGTGACCTGGCGGCGACCTGGTGGCTGAC 158
 2247 GCGCTCCGCTTAATCTCCCTCTGCTGCTGGGGCCGCCGGCCGGAGGCC 2306

159 GAGGCAGGGCCCTCTACAGGACAGAGTCGGCCGGCTCACCTGACGGCTGGCGAT 218
 2307 CGCGCCTGGGAGCGACCCGACGGCGCCCTATGCTGCGGGGGCGCGCGCTC 2366

219 CCCGACTCTGCGCGGGCICCCGACAGATGACGCGCTGTCAGATCGTGGAGGA 278

RESULT 6
 US-09-917-800A-1527
 Sequence 1527, Application US/09917800A
 ; Parent No. US2002019462A1
 ; GENERAL INFORMATION:
 APPLICANT: Mendrick, Donna
 APPLICANT: Porter, Mark
 APPLICANT: Johnson, Kory
 APPLICANT: Castle, Arthur
 APPLICANT: Elashoff, Michael
 APPLICANT: Gene Logic, Inc.
 TITLE OF INVENTION: Molecular Toxicology Modeling
 FILE REFERENCE: 44921-5038-US
 CURRENT APPLICATION NUMBER: US/09/917,800A
 CURRENT FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: US 60/222,040
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: US 60/292,880
 PRIOR FILING DATE: 2000-11-02
 PRIOR APPLICATION NUMBER: US 60/290,029
 PRIOR FILING DATE: 2001-05-11
 PRIOR APPLICATION NUMBER: US 60/290,645
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: US 60/292,336
 PRIOR FILING DATE: 2001-05-22
 PRIOR APPLICATION NUMBER: US 60/295,798
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: US 60/297,457
 PRIOR FILING DATE: 2001-06-13
 PRIOR APPLICATION NUMBER: US 60/298,884
 PRIOR FILING DATE: 2001-06-19
 PRIOR APPLICATION NUMBER: US 60/303,459
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 1740
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1527
 LENGTH: 1366
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 FEATURE: OTHER INFORMATION: Genbank Accession No. US20020119462A1 227118
 US-09-917-800A-1527

Query Match 6.3%; Score 44.6; DB 10; Length 1366;
 Best Local Similarity 47.6%; Pred. No. 0.24; Mismatches 131; Conservative 0; Indels 0; Gaps 0;

QY 95 CGCGCTCCGCCACTTACAGTTCTGGACCTGGCGTGGCAGCTGGCTCC 154
 Db 363 CGCAGCGCAGGCCAACAAAGCAGCGGGCGATGCGGCTGACGTCGCGATA 422
 QY 155 TGACGGAGGGGCCCTACAGGACAGCTGGCGCTAACCTGACCCGCTA 214
 Db 423 TCAAGGAGCCACGCGGCCATGCGTACGGCTGGACGGAGGGCGAGCGAGC 482
 QY 215 GCATCCCGACTCTGCGCCGCCGACCGATGACCGCTGCGCAGATGCTG 274
 Db 483 GCAAGGTGCTCATCTGCGACCTGGGGTGGCACCTGAGCTGTCATCTGACGATCG 542
 QY 275 ACGAGGCAACGAGGGAGGGCTGGAGTCACAGTCGCTGCGCTTGCGCA 334
 Db 543 ACGGCGCATCTGAGGTGAAGSCACSGCGCGACAGCGACCTGGCGGGAGGACT 602
 QY 335 CTGGGACCATGCTGGCTGTTACCTGGTGAAGGAG 369

Db 603 TGGACACCCGGTGGTGAGCCACTTCGTTGGAGGAG 637

RESULT 7

; Sequence 7, Application US/09917800A

; Patent No. US2002119462A1

; GENERAL INFORMATION:

; APPLICANT: Mendrick, Donna

; APPLICANT: Porter, Mark

; APPLICANT: Johnson, Kory

; APPLICANT: Castle, Arthur

; APPLICANT: Elashoff, Michael

; TITLE OF INVENTION: Gene Logic, Inc.

; Molecular Toxicology Modeling

; FILE REFERENCE: 4421-5038-US

; CURRENT APPLICATION NUMBER: US/09/917,800A

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/222,040

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880

; PRIOR FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: US 60/230,029

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: US 60/290,645

; PRIOR FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: US 60/292,336

; PRIOR FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: US 60/295,798

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: US 60/297,457

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/298,884

; PRIOR FILING DATE: 2001-06-19

; PRIOR APPLICATION NUMBER: US 60/303,459

; PRIOR FILING DATE: 2001-07-09

; NUMBER OF SEQ ID NOS: 1740

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1386

; LENGTH: 2455

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE: OTHER INFORMATION: Genbank Accession No. US2002119462A1 L16764

US-09-917-800A-1386

Query Match

Best Local Similarity 6.3%; Score 44.6; DB 10; Length 2455;

Matches 131; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 95 CGCGGCTCCCCCCCCTACTACGTTCTGTGTTGACCTGGGCTTGCGCACCTGGTGTGCC 154

Db 635 CGCAGGGCAGGCCACCAAGGACGGCGGGCGATCTGGGGTGTGAACGTCGCTGGGATCA 694

Qy 155 TACCGGAGCGGCCGCGCCCTCAAGGCACAGCTGGCGCATCGCTATGGCTGGACCGGGAGGGAGC 754

Db 695 TCAACGGAGCCAAAGGGCGGCCATCGCTATGGCTGGACCGGGAGGGAGC 754

Qy 215 GCATCCCGACTCTGCCCGGCCGACAGATGACGCCCTGTCGAGATCGGG 274

Db 755 GCAACGCGTCTCATCTTGACCTGGGGGGCGCACGTTGACCTGGTCATCCGTGACCATCG 814

Qy 275 AGGAGGCCAACGACGGGAGGGCTGGGACTGCTGCTGGGCTTGCGCGCA 334

Db 815 AGGAGCGCATCTCGAGGTGAAGGCCACGGGGCACACGCCACTGGCGGGAGGACT 874

Qy 335 CTTGGCACCATGCTGGCTGTTGACCTGGTGAAGGAG 369

Db 875 TCGACACCCGGTGGTGAAGCCACTTCGTTGGAGGAG 909

RESULT 8

; Sequence 8, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Hasselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zuskind, Judith W.

; APPLICANT: Walz, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

; FILE REFERENCE: ELTRIA 011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,777

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: Fastaseq for Windows Version 4.0

; SEQ ID NO 7988

; LENGTH: 1680

; TYPE: DNA

; NAME/KEY: CDS

; FEATURE: Pseudomonas aeruginosa

; ORGANISM: Pseudomonas aeruginosa

; NAME/KEY: CDS

; LOCATION: (1)..(1680)

US-09-815-242-7988

Query Match

Best Local Similarity 54.2%; Pred. No. 0.28; Mismatches 76; Indels 0; Gaps 0;

Matches 90; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 125 TGGACCTGGCTGGGCCACCTGGTGTCCCCGACGGAGCGGGCCCTCACAGGCCACA 184

Db 533 TGGGGCTGGCTGGGCCACCTGGTGTCCCCGACGGAGCGGGCCCTCACAGGCCACA 592

Qy 185 GCCTGGCCGCCACCCGGTGTCCCCGACGGAGCGGGCCCTCACAGGCCACA 244

Db 593 GCCAGCAGGCCACGACTTCGGCTGGCGATCGCTACGGAGGCCAAGG 652

Qy 245 ACCAGATGACGCCCTGGTGCAGATGGGGAGGCCAAGGCCAG 290

Db 653 ACCTGGGACGCCCTGGCGCGATCCAGCGCTACACGCCAAGG 698

RESULT 9

; Sequence 9, Application US/09758269

; Sequence 13, Application US/09758269

; Patent No. US20020104120A1

; GENERAL INFORMATION:

; APPLICANT: IUCHI, SATOSHI

; APPLICANT: KOBAYASHI, MASATOMO

; APPLICANT: SHINONOKI, KAZUO

; TITLE OF INVENTION: TRANSGENIC PLANTS CARRYING NEOXANTHIN

; TITLE OF INVENTION: CLEAVAGE ENZYME GENE

; FILE REFERENCE: 3314-3

; CURRENT APPLICATION NUMBER: US/09/758,269

; CURRENT FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: JP 2001-003476

; PRIOR FILING DATE: 2001-01-11

US-09-815-242-7988

PRIOR APPLICATION NUMBER: JP 2000-010056
 PRIOR FILING DATE: 2000-01-13
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 13
 LENGTH: 1815
 TYPE: DNA
 ORGANISM: zea mays
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: (1)..(1812)
 US-09-758-269-13

Query Match 6.2%; Score 43.8; DB 10; Length 1815;
 Best Local Similarity 50.7%; Pred. No. 0.39; 0; Mismatches 102; Indels 0; Gaps 0;
 Matches 105; Conservative 0;

Qy 79 CGGGACTGCGCAGCCGGCTCCCCCACATACAGAGTCTCTTGACCTGGCG 138
 Db 592 CGGCCCTCGCCAGAGCGCGATCGCCCAAGGGCATGGCGAG 651
 Qy 139 CGGAACTGTGTCTGAGGGAGGGGGCCCTACAGAGCAGTCGCCGC 198
 Db 652 CTGCAAGGCCACTCGGGATGGCGCCCTGCCCTGTCTACGGCGCCGGCG 711
 Qy 199 ACCGACACGCCCTCGCCGGCACCGCGTGCACGGCGCCGGCG 258
 Db 712 CTGTTGACCCCTCGCCGGCACCGCGTGCACGGCGCCGGCG 771
 Qy 259 TTCTTGACATCGTGACAGGGCCAC 285
 Db 772 CGCCGCTCGCCATGTCGGAGGAC 798

RESULT 10
 US-09-778-927A-16/c
 ; Sequence 15, Application US/09778927A
 ; GENERAL INFORMATION:
 ; APPLICANT: KHOSRAV, Rami et al.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
 ; FILE REFERENCE: 2786-0160P
 ; CURRENT FILING DATE: 2001-02-08
 ; PRIORITY APPLICATION NUMBER: IL134453
 ; PRIORITY FILING DATE: 2000-02-09
 ; PRIORITY APPLICATION NUMBER: IL135341
 ; PRIORITY FILING DATE: 2000-03-23
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 15
 ; LENGTH: 4282
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc_feature
 ; LOCATION: (1)..(4282)
 ; OTHER INFORMATION: n = a, c, g, t any unknown or other
 ; US-09-778-927A-16

Query Match 6.2%; Score 43.6; DB 10; Length 4282;
 Best Local Similarity 46.6%; Pred. No. 0.56; 0; Mismatches 139; Conservative 0; Indels 0; Gaps 0;
 Matches 139; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

Qy 36 CGTGCAGCCCCAACCTTCCTGGTGTCGGAGCCGACTGGGGAGCTGGGCC 95
 Db 714 CCTGCTCCACACGGCGCAGCGCTGGCGACCGCGCTGGCGCTGGGCC 655
 Qy 96 GCGGCCTCCGCCACTACCAAGTTCCTGTGGACCTGGCGCTGGCGACTGGTCCC 155
 Db 654 GCGGAGACGCCAACCACTGGCGACGAGCTCGACAGGCCCTGACCTTGCTT 595
 Qy 156 GACSGAGCGGGCCCTACACGAGACTGGCCGCCTCACCTTCACCGCTGG 215
 Db 594 GGCGCGCACAGCTCTCTCGCTCACACGCCGCCGCCGCCGCCAGCTCCC 535
 Qy 216 CATCCCGACTCTCCCCGGGCCCCAACAGATCGACCGCTTGTCAGATGTGGA 275
 Db 534 GCTCCAGCCAGCGCCAGCGCGCCGCCGCGCCAGCTGCCGCTTGCGCC 475
 Qy 276 CGAGGCCAAGCAGCGAGGGAGGGCTGGAGTGCCTGCTCTGGGTTGGCGC 333
 Db 474 GCTCTCCACTGTGGGGCGGCCATCCAGCCCTGCTGGACCCGGGGCGCTC 417

RESULT 11
 US-10-044-090-668/c
 ; Sequence 668, Application US/10044090
 ; Patent No. US20020137081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olga Bandman
 ; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
 ; FILE REFERENCE: PA-0028 US
 ; CURRENT APPLICATION NUMBER: US20020137081A1
 ; CURRENT FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 850
 ; SOFTWARE: PERL Program
 ; SEQ ID NO: 668
 ; LENGTH: 4366
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20020137081A1 319136.21
 ; NAME/KEY: unsure
 ; LOCATION: 3345-3660
 ; OTHER INFORMATION: a, t, c, g, or other
 ; US-10-044-090-668

Query Match 6.2%; Score 43.6; DB 12; Length 4366;
 Best Local Similarity 46.6%; Pred. No. 0.56; 0; Mismatches 139; Conservative 0; Indels 0; Gaps 0;
 Matches 139; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

Qy 36 CGTGCAGCCCCAACCTTCCTGGTGTCGGAGCCGACTGGGGAGCTGGGCC 95
 Db 714 CCTGCTCCACACGGCGCAGCGCTGGCGACCGCGCTGGCGCTGGGCC 655
 Qy 96 GCGGCCTCCGCCACTACCAAGTTCCTGTGGACCTGGCGCTGGCGACTGGTCCC 155
 Db 654 GCGGAGACGCCAACCACTGGCGACGAGCTCGACAGGCCCTGACCTTGCTT 595
 Qy 156 GACSGAGCGGGCCCTACACGAGACTGGCCGCCTCACCTTCACCGCTGG 215
 Db 594 GGCGCGCACAGCTCTCTCGCTCACACGCCGCCGCCGCCGCCAGCTCCC 535
 Qy 216 CATCCCGACTCTCCCCGGGCCCCAACAGATCGACCGCTTGTCAGATGTGGA 275
 Db 534 GCTCCAGCCAGCGCCAGCGCGCCGCCGCGCCAGCTGCCGCTTGCGCC 475
 Qy 276 CGAGGCCAAGCAGCGAGGGAGGGCTGGAGTGCCTGCTCTGGGTTGGCGC 333
 Db 474 GCTCTCCACTGTGGGGCGGCCATCCAGCCCTGCTGGACCCGGGGCGCTC 417

RESULT 12
 US-09-764-860-768
 ; Sequence 768, Application US/09764860
 ; Patent No. US20020094953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC008
 ; CURRENT APPLICATION NUMBER: US/09/764, 860
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1198
 SOFTWARE: PatentIn ver. 2.0
 SEQ ID NO: 768
 LENGTH: 6000
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-764-860-768

Query Match 6.1%; Score 42.8; DB 10; Length 6000;
 Best Local Similarity 50.5%; Pred. No. 0.93; Mismatches 102; Indels 0; Gaps 0;
 Matches 104; Conservative 0;

Qy 125 TGGACCTGGGGTGGGACCTGGGTTCTGACGGAGCGGGCCCTCACAGGACA 184
 Db 169 CCGACTGGCTGACCCTGCTACAGCAGCAACAGGGCTAGTCAGTCCTCT 228
 Db 185 GCTGCCCGGCTCACCTGACCCGCTGGCATCCCGACTTCAGCCCCCGGGCCCG 244
 Db 229 GCGGCCCTGCACGCCCTCACCTCTCTCTGCCCTGGGGCCACCGCTACG 288

Qy 185 GCTGCCCGGCTCACCTGACCCGCTGGCATCCCGACTTCAGCCCCCGGGCCCG 184
 Db 287 TGGCCACGCCATGGATCGGGCTCCGAGATGAGGGCTAGTCATGGAC 2926

Qy 185 GCTGCCCGGCTCACCTGACCCGCTGGCATCCCGACTTCAGCCCCCGGGCCCG 244
 Db 2927 GCAATGGCTCGTGGAGCGCATGGGCTCCGGATAGGGCAATGGCCGCTCG 2986

Qy 245 ACCAGATCGACGCCATGGGTGGGCTGG 304
 Db 2987 ACCACATGGCTCAGCATGGGCCAGACCATGGGCAATGGCTGGCG 3046

Qy 305 GAGTGCACCTGGCTGGGTTGGCCAC 330
 Db 3047 TGGAGCGCATGGTCCGGCATGGG 3072

RESULT 13
 DS-09-747-835A-10
 Sequence 10, Application US/09747835A
 Patent No. US2002014682A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
 APPLICANT: Yamazaki, Victoria
 APPLICANT: Liu, Chenghua
 APPLICANT: Zhou, Ping
 APPLICANT: Wang, Dunrui
 APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyun
 APPLICANT: Asundi, Vinod
 APPLICANT: Drmanac, Radivoj T

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
 TITLE OF INVENTION: LIE POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: HYS-27CIP

CURRENT APPLICATION NUMBER: US/09-747, 835A

CURRENT FILING DATE: 2002-03-08

PRIOR APPLICATION NUMBER: US 09/729, 739
 PRIOR FILING DATE: 2000-12-04

PRIOR APPLICATION NUMBER: US 09/653, 450
 PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: US 09/620, 312
 PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: US 09/598, 042
 PRIOR FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: US 09/552, 317
 PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 09/488, 725
 PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 63
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 10
 LENGTH: 391
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-747-835A-10

Query Match 6.0%; Score 42.2; DB 10; Length 1347;
 Best Local Similarity 46.0%; Pred. No. 0.81; Mismatches 143; Indels 168; Gaps 0;
 Matches 143; Conservative 0;

Qy 20 CTTCGCCGCGCTGGGCTGACGCCCAACTCTCTGGGCTTCGGCCGGCTGG 79
 Db 1277 CTTCGCCGCGCTGGGCTGACGCCCAACTCTCTGGGCTTCGGCCGGCTGG 1218

Qy 80 CGGACTGCGCTCCGGCACTACGACGCGCTGGACCTGGCG 139
 US-09-815-242-7912/C
 Sequence 7912, Application US/09815242
 Patent No. US2002006169A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
 TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.01IA

CURRENT APPLICATION NUMBER: US/09-815, 242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191, 078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206, 848

PRIOR FILING DATE: 2000-03-23

PRIOR APPLICATION NUMBER: 60/207, 727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242, 578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/233, 625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257, 931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269, 308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 1410
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 7912
 LENGTH: 1347
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(1347)
 US-09-815-242-7912

Query Match 6.0%; Score 42.2; DB 10; Length 1347;
 Best Local Similarity 46.0%; Pred. No. 0.81; Mismatches 143; Indels 168; Gaps 0;
 Matches 143; Conservative 0;

Qy 80 CGGACTGCGCTCCGGCACTACGACGCGCTGGACCTGGCG 139

Db 1217 CGGACTCTGCTTGCCAGCGTTCGAGCGACACAGGGTACGGGTGCCAGTCCTGG 1158
 Qy 140 CGCACCTGGTCTCCCTGACGGAGCGGGCCCCCTACAGGGACAGCTGCCGGCTCA 199
 Db 1157 GCAATCAGGCCGCGTCAGCAGCTACCGCCGGAGAAGGCCGACCGGG 1098
 Qy 200 CCTGACCGCATCCGACTCTGCTGCCGCGCCGCCCCGACCATCGACGCT 259
 Db 1097 TCGCGGAGGTCATGGAATCGGCCCTGCGCTCTCGCGGAGCAGCCTG 1038
 Qy 260 TCGTGCAGAGCTGGACGAGGCCAACGGAGGGCTGGGAGTCACATGCTC 319
 Db 1037 CGTCGAGTGGCACCCAGGCCCTGATGCCAGGGCGCGACGTGGGGCC 978
 Qy 320 TGGCTTGCC 330
 Db 977 TTGGATCGTC 967

Qy 305 GAGTCACCTGCTCTGGCTTGG 329
 Db 274 TCGAGCNCAIGGGTCCGGCATGG 298

Search completed: November 4, 2002, 10:23:40
 Job time : 65 secs

RESULT 15

US-09-759-143-399

; Sequence 399, Application US/09/59143

; Patent No. US200202248A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Devin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedula, Thomas S.

; APPLICANT: Carter, Barrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Ajun

; APPLICANT: Skeky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C23

; CURRENT APPLICATION NUMBER: US/09/759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 399

; LENGTH: 298

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(298)

; OTHER INFORMATION: n = A,T,C or G

; US-09-759-143-399

; Query Match 5..9%; Score 42; DB 10; Length 298;

; Best Local Similarity 49..8%; Pred. No. 0..57; Mismatches 0; Indels 0; Gaps 0;

; Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

; Qy 125 TGGACCTGGCGTGGGACCTGGGCTCTGAGGGAGGGGGCCCCCTCACAGCGACA 184

; Db 94 TGGGCCACGGCATGGATCGCGTGGGCCGCTCCGAGTCGAGGCCATGGCTATGGACC 153

; Qy 185 GCTGCCCGGCCCTACCCCTACCCCTGGCATCCGACTCTGGCGGGGGGGGGGGGG 244

; Db 154 GCAGGGCGTGGGAGGCCATGGCTGGGCTGGGAGTCGAGGCCATGGCTATGGACC 213

; Qy 245 ACCAGATCGACCGCTCTGGCAGATGGTGGACGAGGCCAACGGCAGCGACGGGAGAGCTGGG 304

; Db 214 RCCATGGCCCTCCANCATGGCCATGGCCAGACCATGGAGGGCATGGCTCTGGCG 273

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Gencore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 4, 2002, 07:57:17 ; Search time 52 Seconds
(without alignments)

Scoring table: IDENTITY_NUC Gopop 10.0 , Gapext 1.0

Title: US-09-619-380-1

Perfect score: 707

Sequence: 1 tgacccgtgcctgtgcc...aaaaaaaaaaaaaaaaaaa 707

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cn2_6/podata/1/na/5A_COMB.seq:*

2: /cn2_6/podata/1/na/5B_COMB.seq:*

3: /cn2_6/podata/1/na/5A_COMB.seq:*

4: /cn2_6/podata/1/na/6B_COMB.seq:*

5: /cn2_6/podata/1/na/5CUTUS_COMB.seq:*

6: /cn2_6/podata/1/na/backfile1.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.2	7.8	1145	1	US-09-482-385A-1
2	55.2	7.8	2728	1	US-09-482-385A-5
3	46.2	6.5	642	3	US-09-918-853-12
4	46.2	6.5	642	4	US-09-479-409-12
5	46.2	6.5	642	4	US-09-479-453-12
6	46.2	6.5	17612	3	US-09-918-853-29
7	46.2	6.5	17612	4	US-09-479-409-29
8	46.2	6.5	17612	4	US-09-479-453-29
9	45.4	6.4	1926	4	US-09-249-585A-2
10	45.4	6.4	2580	3	US-09-863-2
11	45.4	6.4	2580	4	US-09-359-081-2
12	45.4	6.4	5452	2	US-09-130-114-1
13	45.4	6.4	9600	4	US-09-910-647-1
14	45.4	6.4	9600	4	US-09-620-925-1
15	45.4	6.4	10596	1	US-07-884-811-15
16	45.4	6.4	10596	1	US-08-804-971-15
17	45.4	6.4	10596	1	US-08-087-783A-15
18	45.4	6.4	10596	1	US-08-194-088B-15
19	45.4	6.4	10596	2	US-08-194-088B-15
20	45.4	6.4	10596	5	PCT-US93-04648-15
21	44.8	6.3	44377	2	US-08-804-227C-7
22	44.8	6.3	44377	2	US-08-804-198-1
23	44.8	6.3	4403765	4	US-09-103-840A-2
24	44.2	6.3	9960	3	US-08-822-586-46
25	44.2	6.2	833	2	US-08-403-620-3
26	44.2	6.2	833	3	US-08-510-646B-3
27	44.2	6.2	833	4	US-09-231-818-3

ALIGNMENTS

RESULT	1
US-08-482-385A-1	; Sequence 1, Application US/08482385A
	; Patent No. 5728561
	; GENERAL INFORMATION:
	; APPLICANT: DENOYA,, CLAUDIO D.
	; TITLE OF INVENTION: GENES ENCODING BRACHED CHATN ALPHA
	; NUMBER OF SEQUENCES: 15
	; CORRESPONDENCE ADDRESS:
	; ADDRESSEE: PETER C. RICHARDSON
	; STREET: 235 EAST 42ND STREET, 20TH FLOOR
	; CITY: NEW YORK
	; STATE: NEW YORK
	; COUNTRY: U.S.A.
	; ZIP: 10017-5755
	; COMPUTER READABLE FORM:
	; COMPUTER: IBM PC compatible
	; OPERATING SYSTEM: PC-DOS/MS-DOS
	; SOFTWARE: Patentin Release #1.0, Version #1.25
	; CURRENT APPLICATION DATA:
	; APPLICATION NUMBER: US/08/482-385A
	; FILING DATE: 07-JUN-1995
	; CLASSIFICATION: 435
	; ATTORNEY/AGENT INFORMATION:
	; NAME: SHEVKA,, ROBERT F.
	; REGISTRATION NUMBER: 31,304
	; REFERENCE/DOCKET NUMBER: PC8346C
	; TELECOMMUNICATION INFORMATION:
	; TELEPHONE: 212-573-1189
	; TELEFAX: 212-573-1939
	; INFORMATION FOR SEQ ID NO: 1:
	; SEQUENCE CHARACTERISTICS:
	; LENGTH: 1145 base pairs
	; TYPE: nucleic acid
	; STRANDEDNESS: double
	; TOPOLOGY: linear
	; MOLECULE TYPE: cDNA
	; US-08-482-385A-1
	Query Match Best Local Similarity 7.8%; Score 55.2; DB 1; Length 1146; Matches 141; Conservative 49.6%; Pred. No. 0.0065; Indels 0; Gaps 0;
Qy	55 CCTCGGGTGTCTCGGGCGCGTACTGGCGTCCTCCGCCACTAAC 115
Db	260 CCTCGGGTGTCTCGGGCGCGTACTGGCGTCCTCCGCCACTAAC 319
Qy	116 AGTTCCTGTTGGACCTGGGCGTGCGGCACCTGGTGTCCCTGACGGAGCGCGACTCTCCCCAGCTAC 175

RESULT 2
US-08-482-385A-5
Sequence 5, Application US/08482385A

GENERAL INFORMATION:
 APPLICANT: DEMOYA, CLAUDIO D.
 TITLE OF INVENTION: GENES ENCODING BRACHED CHAIN ALPHA KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES

NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PETER C. RICHARDSON
 STREET: 235 EAST 42ND STREET, 20TH FLOOR
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10017-5755

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482, 385A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: SHEYKA, ROBERT F.
 REGISTRATION NUMBER: 31, 304
 REFERENCE/DOCKET NUMBER: PC8346C

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-573-1189
 TELEFAX: 212-57-1939
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2728 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-482-385A-5

Query Match 7.8%; Score 55.2; DB 1; Length 2728;
 Best Local Similarity 49.6%; Pred. No. 0.0008; Matches 141; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 56 CCTGGGTTCTCCGGGCGACTGGGACTGGGCTGCCGCGCTCCGGCCACTTAC 115
 Db 662 CCTGGGAGGTGGCCGCCGCTCTGCTGGAGACGGCGACTGGCTCTCCAGCTAC 721

QY 116 AGTCCTCTGGACCTGGGGCGAACCTGGCTCTGAGGGCGGGCCCCCTC 175
 Db 722 GGACACCCCTGGCCGCGCTGCGATCCGGCTCACCTCTG 781

Db 176 ACAGACAGCTGGCCGGCTCACCTGGACCGCGCTCCGACTTCTGCCG 235
 QY 500 AGCAGTGGAGTGACTGTCTCTGGCTTGGCGACTGGCAGCTGGC 339

QY 236 CGGCCCGGACGAGATGAGCGCTTGGCAAGATGTTGAGAGGCCAACGGAG 295
 Db 842 CTCTCGGACGCCAGCTCCGCACGGCGCTGGCGACGGCGCCCTCAAGGGCG 901

QY 296 AGCTGTGGAGTGACTGTCTCTGGCTTGGCGACTGGC 339
 Db 902 ACGACGTGGCTGGCCCTGGCTGGCGACGGGACAGCAG 499

RESULT 3
US-08-911-853-12
Sequence 12, Application US/08911853

GENERAL INFORMATION:
 APPLICANT: Gerritse, Gijsbert
 APPLICANT: Ouak, Wilhelmus J.
 TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genencor International
 STREET: 925 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1013

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/911, 853
 FILING DATE: 16-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Glaisier, Debra J.
 REGISTRATION NUMBER: 33, 888
 REFERENCE/DOCKET NUMBER: GC361-2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-846-7620
 TELEFAX: 650-845-6504
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 642 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-911-853-12

Query Match 6.5%; Score 46.2; DB 3; Length 642;
 Best Local Similarity 48.0%; Pred. No. 0.061; Matches 132; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 4 CCCGCTGCTTGTGCGCTTCCAGGATGGCGTGGAGGCCAACCTCTCCGGG 63
 Db 67 CTGGGGTGGCTCATCCCTAGCGTACAGAGCATGACTCTGGCTC 126

QY 64 CTTCGGGGCGCTGGGAGACTGGGCTGCCGCGCTCCGGCCACTACAGCTTG 123
 Db 127 CTGGGAGGCGGCCACGGCGCCAGAGAGATCGCGAGGCCAGCGCTG 186

QY 124 TTGGACCTGGCTGGGAGCTGGGCTGGCTGGGCTGGGCTGGGCTGGG 183
 Db 187 TCCATCAGGCGCTGAGCATCTGTCGCGACGGCGGGGACCGAG 246

QY 184 AGCTGCCGCGCTTACCCCTGGCGCTGGCATGCCACTTGTGCCGCC 243
 Db 247 GCGGCGCCACCGGGAGCAGATGAGCTGTGGCGAGCTGTGCA 306

QY 244 GACCAGATCGACCGCTTCGAGATCGTGGGACGA 278

RESULT 4 ; US-09-479-409-12
; Sequence 12, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerrisse, Gijssbert
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 642 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-479-409-12
; Query Match 6.5%; Score 46.2; DB 4; Length 642;
; Best Local Similarity 48.0%; Pred. No. 0.061; Gaps 0;
; Matches 132; Conservative 0; Mismatches 143; Indels 0;
; Gaps 0;
; QY 4 cccgcgcgtccgtggccgttccagcgatggcggtgcacggcccaactctccgtggcg 63
; Db 67 cttcggtgggtgttcgtccatcacccgtcagcgatggcggtgcacggccacttcgttgcgtg 126
; Qy 64 cttccggccggctggcgatgtggcggtcccgccactaccasgtccgt 123
; Db 127 ctggccatgcggccggccacggccccccatggaggatcgccggaggcccggccgtg 186
; Qy 124 ttggacctgggtgcgcacccgtgtgtccgtacggagcgccggccctcacagcgac 183
; Db 187 tccatccaggccgtcgacatcggtcgacggccggccaggccggccgaccag 246
; Qy 184 agctggccggccgtcacccgtggccgtggcatccccactctggccgtggcg 243
; Db 247 ggcgcgcggccacccggcaggatgtggcgatccggcc 278
; Qy 307 aaggccgtccacggcgatcatccagggtccggcc 341
; US-09-479-453-12
; Query Match 6.5%; Score 46.2; DB 4; Length 642;
; Best Local Similarity 48.0%; Pred. No. 0.061; Gaps 0;
; Matches 132; Conservative 0; Mismatches 143; Indels 0; Gaps 0;
; Gaps 0;
; Qy 4 cccgcgcgtccgtggccgttccagcgatggcggtgcacggcccaactctccgtggcg 63
; Db 67 cttcggtgggtgttcgtccatcacccgtcagcgatggcggtgcacggccacttcgttgcgtg 126
; Qy 64 cttccggccggctggcgatgtggcggtcccgccactaccasgtccgt 123
; Db 127 ctggccatgcggccggccacggccccccatggaggatcgccggaggcccggccgtg 186
; Qy 124 ttggacctgggtgcgcacccgtgtgtccgtacggagcgccggccctcacagcgac 183
; Db 187 tccatccaggccgtcgacatcggtcgacggccggccaggccggccgaccag 246
; Qy 184 agctggccggccgtcacccgtggccgtggcatccccactctggccgtggcg 243
; Db 247 ggcgcgcggccacccggcaggatgtggcgatccggcc 278
; Qy 307 aaggccgtccacggcgatcatccagggtccggcc 341
; RESULT 6 ; US-09-479-453-12
; Sequence 12, Application US/09479453
; Patent No. 6313283
; GENERAL INFORMATION:
; APPLICANT: Gerrisse, Gijssbert
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,453
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 642 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

RESULT 5

Page 3

APPLICANT: Quax, Wilhelmus J.
 TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genencor International
 STREET: 925 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94041-1013
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/911,853
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/699,092
 FILING DATE: 16-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Glaister, Debra J.
 REGISTRATION NUMBER: 33,888
 REFERENCE/DOCKET NUMBER: GC361-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-846-7620
 TELEFAX: 650-845-6504
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17612 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; US-08-911-853-29
 Query Match 6.5%; Score 46.2; DB 3; Length 17612;
 Best Local Similarity 48.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
 Matches 132; Conservative 0; MisMatches 143; Indels 0; Gaps 0;
 QY 4 CCGCTCTGCTGTGGCCCTTCCCAGCGAAGGGGGCAGCCCCCAACTTCCTGGGG 63
 Db 4085 CTGGTGGTGCTGCTCATACCCCTAGCCAGAACATGACTTCCTGGCTG 4026
 QY 64 CTTCGGGGGGCTGGGGACTGGCTTCCGGCTCCGGCCACTACCGATCTG 123
 Db 4025 CTGGCAGGGAGGCCACCCGGCCAGAGATCGCGAGGCCACCGCTG 3956
 QY 124 TTGGACCTGGGGGGGGGACCTGGTCTGAGGGAGGGGGCCCTCACAGCGAC 183
 Db 3965 TCCATCCAGGCCTCAGCTGTCTGGCACGCCGGCCAGGGCGGCCAGGACAG 3906
 QY 184 AGCTGGCCGGCTCACCCGCAACGGCTGGCAATCCCGACTTCGGCCGG 243
 Db 3905 GCGGCCGCCACCGGGAGAGATGACCTGCTGGCAAGCTGGCCAGGCC 3846
 QY 244 GACCGATGACCGCTTCGGAGATGACCTGGCTGTCACCCGGAGCC 278
 Db 3845 AAGCGCTCACGGGATCATCGCAGGGGA 3811
 RESULT 8
 US-09-479-453-29/C
 ; Sequence 29, Application US/09479453
 ; General Information:
 ; Patent No. 613283
 ; APPLICANT: Gerritse, G.J.
 ; APPLICANT: Quax, Wilhelmus J.
 ; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genencor International
 ; STREET: 925 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA

RESULT 7
 US-09-479-409-29/C
 ; Sequence 29, Application US/09479409
 ; General Information:
 ; Patent No. 6225106
 ; APPLICANT: Gerritse, G.J.
 ; APPLICANT: Quax, Wilhelmus J.
 ; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:

TITLE OF INVENTION: Polynucleotide Delivery
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
Country: U.S.A.
ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,647
FILING DATE:
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459

REFERENCE/DOCKET NUMBER: 1218.002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 923-2106
TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 9600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
8-910-647-1

COUNTRY: U.S.A.
ZIP: 94008-2916
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/620,925
FILING DATE: 21-JUL-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,647
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Search completed: November 4, 2002, 09:26:53
Job time : 138 secs

GenCore version 5.1.3
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ALIGNMENTS

OM protein - protein search, using sw model
Run on: November 4, 2002, 12:49:58 ; Search time 33 Seconds
Sequence: 1 MGVQPPNFSWVLPGRLAGLA.....GSIETVEQEKAVFQYORTK 150
Scoring table: ORIGO Gapop 60.0 , Gapext 60.0
Searched: 908470 seqs, 133550620 residues
Total number of hits satisfying chosen parameters: 10~
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Listing first 45 summaries

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 21: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA2001.DAT: *
 22: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA2002.DAT: *
 23: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA2003.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Match	Query	Length	DB	ID	Description
	1	150	100.0	150	22	AAB03228	Human protein phosphatase
	2	150	100.0	150	22	AAB35275	Human dual specific phosphatase
	3	150	100.0	179	23	ABP3078	Human ovarian anti-phosphatase
	4	131	87.3	150	22	AAB3231	Human phosphatase
	5	131	87.3	150	22	AAB3231	Amino acid sequence
	6	131	87.3	150	22	AAG67634	Amino acid sequence
	7	131	87.3	150	23	ABB07846	Human tyrosine phosphatase
	8	23	33	150	22	AAB93211	Murine phosphatase
	9	35	23.3	150	22	AAB35276	Murine dual specific phosphatase
	10	21	22	14.0	22	AAB35273	Human dual specific phosphatase

fraction of total tissues expressing PPmK-P γ) include reproductive (0.372), cardiovascular (0.140) and endocrine (0.093). Diseases or conditions associated with tissues expressing PPmK-P γ (as a fraction of total tissues expressing PPmK-P γ) include cancer (0.558), inflammation or trauma (0.233) or cell proliferation (0.209). The encoded protein shows homology to Clona intestinalis tyrosine phosphatase. The invention provides human PPmK-P γ to -11 polypeptides (see AB2022-32) and polynucleotides (see AB30476-86). It also provides expression vectors, host cells, antibodies, agonists and antagonists, as well as methods for diagnosing, treating or preventing disorders associated with expression of PPmK, including gastrointestinal disorders, immune system disorders, neurological disorders and cell proliferative disorders, including cancer.

Sequence 150 AA;

Query Match	Score	DB	Length	Matches	Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
QY 1 MGVOPPNFSWVLRGLALPRLPAHYQLLDLGYRHVLSLTERGPSPSDCPGLTHR 60	100.0%	DB 22	150	150; Conservative	100.0%	Pred.	1e-145;	0;	0;	0;
Db 1 MGVOPPNFSWVLRGLALPRLPAHYQLLDLGYRHVLSLTERGPSPSDCPGLTHR 60										
QY 61 LRIFDCECPAPDQIDRFLVQIVDEANARGAVGVLGAGLGRGTMALCYLVKGGLA 120										
Db 61 LRIPFPCPAPDQIDRFLVQIVDEANARGAVGVLGAGLGRGTMALCYLVKGGLA 120										
QY 121 AIAEIRRRLPGSIETYEQEKAVFOYRKT 150										
Db 121 AIAEIRRRLPGSIETYEQEKAVFOYRKT 150										

RESULT 2

ID	AAB35275 standard; Protein; 150 AA.
AC	AAB35275;
XX	
DT	08-MAY-2001 (first entry)
XX	
DE	Human dual specificity phosphatase DSP-11.
XX	
KW	Human; dual specificity phosphatase; DSP-11; Duchenne muscular dystrophy; MAP-kinase signalling cascade; cell proliferation; cancer; allergy; graft-versus-host disease; autoimmune disease; metabolic disease.
XX	
OS	Homo sapiens.
XX	
PN	WO200105983-A1.
XX	
PD	25-JAN-2001.
XX	
PF	19-JUL-2000; 2000WO-US19710.
XX	
PR	20-JUL-1999; 99US-0144557.
XX	
PA	(CBPT-) CEPTYR INC.
XX	
PT	Luche RM, Wei B;
XX	
DR	WPI; 2001-147348/15.
XX	
N-PSDB;	AAF27958.

Novel dual specificity phosphatase-11 dephosphorylating activated mitogen-activated protein kinase, is used to identify agents inhibiting the enzyme activity and modulate cell proliferation.

Claim 1; Fig 2; 65pp; English.

XX Novel dual specificity phosphatase-11 dephosphorylating activated PT mitogen-activated protein kinase, is used to identify agents inhibiting PT the enzyme activity and modulate cell proliferation.

XX PS: Claim 1; SEQ ID No 4210; 292pp; English.

The present invention provides the protein and coding sequences of the human dual-specificity phosphatase Dsp-11. The protein is involved in the MAP-kinase signalling cascade. The sequences can be used in the diagnosis

CC and treatment of Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth and abnormal cell proliferation. The present sequence is the human Dsp-11 protein.

Sequence 150 AA;

Query Match	Score	DB	Length	Matches	Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
QY 121 AIAEIRRRLPGSIETYEQEKAVFOYRKT 150	100.0%	DB 22	150	150; Conservative	100.0%	Pred.	1e-145;	0;	0;	0;
Db 121 AIAEIRRRLPGSIETYEQEKAVFOYRKT 150										
QY 61 LRIPFPCPAPDQIDRFLVQIVDEANARGAVGVLGAGLGRGTMALCYLVKGGLA 120										
Db 61 LRIPFPCPAPDQIDRFLVQIVDEANARGAVGVLGAGLGRGTMALCYLVKGGLA 120										
QY 121 AIAEIRRRLPGSIETYEQEKAVFOYRKT 150										
Db 121 AIAEIRRRLPGSIETYEQEKAVFOYRKT 150										

RESULT 3

ID	ABP43078 standard; Protein; 179 AA.
AC	ABP43078;
XX	
DT	22-AUG-2002 (first entry)
XX	
DE	Human ovarian antigen HVAJAJ27, SEQ ID NO:4210.
XX	
KW	Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; reproductive system disorder; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
XX	
OS	Homo sapiens.
XX	
PN	WO200200677-A1.
XX	
PD	03-JAN-2002.
XX	
PF	07-JUN-2001; 2001WO-US18569.
XX	
PR	07-JUN-2000; 2000US-209467P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Birse CE, Rosen CA;
XX	
DR	WPI; 2002-147878/19.
XX	
N-PSDB;	ABQ56155.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer); immune disorders, cardiovascular disorders and neurological diseases -

Claim 11; SEQ ID No 4210; 292pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP3228) and to cDNAs encoding them (ABQ5131-ABQ56155), and also encompasses polypeptides 90% identical and Polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to

recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosis or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pot_sequences.

Sequence 179 AA:

Query Match 100.0%; Score 150; DB 23; Length 179;
Best Local Similarity 100.0%; Pred. No. 1; 2e-15;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGVQPPNFSWVLPGRLAGLALRPLPAHYQFLDLGVRHLVSLTERGPSPHSDCPGLIHR 60
Db 30 MGVQPPNFSWVLPGRLAGLALRPLPAHYQFLDLGVRHLVSLTERGPSPHSDCPGLIHR 89
Qy 61 LRIPDFCPAPQDIDRFLQIVDEANANGEAVGVHCAKGFFRGTMACLYLVERGLAGD 120
Db 90 LRIPDFCPAPQDIDRFLQIVDEANANGEAVGVHCAKGFFRGTMACLYLVERGLAGD 149
Qy 121 AIAEIRRRLPESIETYEQEKAVQFORTK 150
Db 150 AIAEIRRRLPESIETYEQEKAVQFORTK 179

RESULT 4

AAB73231
ID AAB73231 standard; Protein: 150 AA.

AC AAB73231;

XX DT 11-MAY-2001 (first entry)

DE Human phosphatase BAA91172.h.

XX KW Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia; cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia; congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease; Moebius syndrome; Bjornstad syndrome; Bannayan-Zonana syndrome; schizophrenia; hamartoma.

XX OS Homo sapiens.
XX PN WO200112819-A2.
XX PD 22-FEB-2001.
XX PR 11-AUG-2000; 2000WO-US22158.
PR 13-AUG-1999; 99US-0149005.
XX PA (SUGE-) SUGEN INC..

RESULT 5

ARG6745
ID ARG6745 standard; Protein: 150 AA.

AC ARG6745;

XX DT 26-NOV-2001 (first entry)

DE Amino acid sequence of a human polypeptide.

XX KW Human; protein kinase; protein phosphatase; signal transduction; KW intracellular signalling pathway.

OS Homo sapiens.

XX PN WO200109345-A1.

XX OS 08-FEB-2001.

XX PN 28-JUL-2000; 2000WO-JP05060.

XX PR 23-JUL-1999; 99JP-0248036.

PR 18-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-018776.

PR 17-FEB-2000; 2000US-0183322.

PR 02-MAY-2000; 2000JP-0183767.

XX PA (HELI-) HELIX RES INST.

PI Plowman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;
XX WPT; 2001-211226/21.
DR DR N-PSDB; RA65583.

PT New protein phosphatase polypeptide for diagnosing and treating phosphatase related disorders such as cancer, schizophrenia, cardiac dysfunction and/or vascular disorders

XX PS Claim 6; Fig 5; 138pp; English.

CC The present invention relates to phosphatase proteins and coding sequences. The present sequence is one such phosphatase. Phosphatases are enzymes that catalyse the dephosphorylation of proteins modified by phosphorylation of serine, threonine or tyrosine residues. For example phosphatases are useful for treating a variety of diseases: For example cancer e.g. breast, urogenital, prostate, head, neck, lung cancers, synovial sarcomas, renal cell carcinoma, non small cell lung cancer, hepatocellular carcinoma, pancreatic endocrine tumours, stomach cancer, glioblastoma, colorectal cancer and thyroid cancer, pathophysiological hypoxia, cardiac dysfunction and/or vascular disorders, myopathies, congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease, ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan-Zonana syndrome, schizophrenia and hamartomas.

Sequence 150 AA:

Query Match 87.3%; Score 131; DB 22; Length 150;
Best Local Similarity 100.0%; Pred. No. 3; 2e-15;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGVQPPNFSWVLPGRLAGLALRPLPAHYQFLDLGVRHLVSLTERGPSPHSDCPGLIHR 60
Db 1 MGVQPPNFSWVLPGRLAGLALRPLPAHYQFLDLGVRHLVSLTERGPSPHSDCPGLIHR 60
Qy 61 LRIPDFCPAPQDIDRFLQIVDEANANGEAVGVHCAKGFFRGTMACLYLVERGLAGD 120
Db 61 LRIPDFCPAPQDIDRFLQIVDEANANGEAVGVHCAKGFFRGTMACLYLVERGLAGD 120
Qy 121 AIAEIRRRLPESIETYEQEKAVQFORTK 131
Db 121 AIAEIRRRLPESIETYEQEKAVQFORTK 131

PI Kossida S;
 XX WPI; 2002-339803/37.
 DR N-PSDB; AAF219563.

XX New human tyrosine phosphatase-like enzyme polypeptide, regulators of which are useful for preventing, treating diabetes, obesity, cancer, cardiovascular and pulmonary diseases -
 PT
 XX
 PS Claim 18; Fig 2; 117pp; English.

XX The invention relates to a purified human tyrosine phosphatase-like enzyme polypeptide. The enzyme can be expressed by standard recombinant methodology. The tyrosine phosphatase-like enzyme and encoding polynucleotides are useful for screening for modulators which are used for treating a tyrosine phosphatase-like enzyme dysfunction related disease such as a central nervous system (CNS) disorder, diabetes, obesity, chronic obstructive pulmonary disease, cardiovascular disease, cancer, anorexia, cachexia, wasting disorders, appetite suppression, and other eating disorder such as bulimia. CNS disorders include brain injuries, Parkinson's disease, dementia, multiple sclerosis, stroke, Alzheimer's disease, Huntington's disease, schizophrenia, Pick's disease, Creutzfeld-Jacob dementia, progressive nuclear palsy, and human immunodeficiency virus (HIV) dementia, pain associated with CNS disorders and cardiovascular diseases include myocardial infarction, ischaemic diseases of the heart, atrial and ventricular arrhythmia, hypertensive vascular diseases and peripheral vascular diseases. The enzyme is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of mutations in the encoding nucleic acid sequences. The present sequence represents the human tyrosine phosphatase-like enzyme polypeptide.

SQ Sequence 150 AA:

Query Match	87.3%	Score	131;	DB	23;	Length	150;			
Best Local Similarity	100.0%	Pred.	No.	3.2e-126;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	131;	Conservative								

QY 1 MGSVOPPNFSWVLPLGRLAGLAPRLPAHQWQLFLDLGVRLVSLTERGPPHSDSCPGLTHR 60
 DO 1 MGVPNPNESWVLPLGRLAGLAPRLPAHQWQLFLDGVRHLVSLTERGPPHSDSCPGLTHR 60

QY 61 LRIIPDFCAPPDDIDRQVIVDANARGEAVGVHCALGFGRGTMACLYLVKER 120
 DO 61 LRIIPDFCAPPDDIDRQVIVDANARGEAVGVHCALGFGRGTMACLYLVKER 120

QY 121 AIAEIRRIRPG 131
 DO 121 AIAEIRRIRPG 131

Sequence 150 AA:

Query Match	23.3%	Score	35;	DB	22;	Length	150;			
Best Local Similarity	100.0%	Pred.	No.	9.6e-28;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	35;	Conservative								

QY 80 IVDEBANARGEAVGVHCALGFGRGTMACLYLVKER 114
 DO 80 IVDEBANARGEAVGVHCALGFGRGTMACLYLVKER 114

RESULT 9
 AAB35276
 ID AAB35276 standard; Protein; 150 AA.
 XX
 AC AAB35276;
 AC
 XX DT 08-MAY-2001 (first entry)
 XX DE Murine dual specificity phosphatase DSP-11.
 XX KW Mouse; dual specificity phosphatase; DSP-11; Duchenne muscular dystrophy; KW MAP-kinase signalling cascade; cell proliferation; cancer; allergy; KW graft-versus-host disease; autoimmune disease; metabolic disease.
 XX OS Mus sp.
 XX PN WO200105983-A1.
 XX PD 25-JAN-2001.
 XX PF 19-JUL-2000; 2000WO-US19710.
 XX PR 20-JUL-1999; 99US-0144557.
 XX PA (CEPT-) CEPTYR INC.
 XX PI Luche RM, Wei B;
 XX DR WPI; 2001-147348/15.
 XX DR N-PSDB; AAF219563.

PI Kossida S;
 XX WPI; 2002-339803/37.
 PR 11-AUG-2000; 2000WO-US22158.
 XX PR 13-AUG-1999; 99US-0149005.
 XX PA (SUGE-) SUGEN INC.
 XX PI Plowman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;
 XX DR WPI; 2001-211226/21.
 DR N-PSDB; AAF63563.

PT New protein phosphatase polypeptide for diagnosing and treating phosphatase related disorders such as cancer, schizophrenia, cardiac dysfunction and/or vascular disorders -
 PT
 XX PS Claim 6; Fig 5; 138pp; English.

CC The present invention relates to phosphatase proteins and coding sequences. The present sequence is one such phosphatase. Phosphatases are enzymes that catalyse the dephosphorylation of proteins modified by phosphorylation of serine, threonine or tyrosine residues. The phosphatases are useful for treating a variety of diseases: for example cancer e.g. breast, urogenital, prostate, head, neck, lung cancers, synovial sarcoma, renal cell carcinoma, non-small cell lung cancer, hepatocellular carcinoma, pancreatic endocrine tumours, stomach cancer, glioblastoma, colorectal cancer and thyroid cancer, pathophysiological hypoxia, cardiac dysfunction and/or vascular disorders, myopathies, congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease, ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan-Zonana syndrome, schizophrenia and hamartomas.

SQ Sequence 150 AA:

Query Match	23.3%	Score	35;	DB	22;	Length	150;			
Best Local Similarity	100.0%	Pred.	No.	9.6e-28;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	35;	Conservative								

QY 80 IVDEBANARGEAVGVHCALGFGRGTMACLYLVKER 114
 DO 80 IVDEBANARGEAVGVHCALGFGRGTMACLYLVKER 114

RESULT 9
 AAB35276
 ID AAB35276 standard; Protein; 150 AA.
 XX
 AC AAB35276;
 AC
 XX DT 08-MAY-2001 (first entry)
 XX DE Murine dual specificity phosphatase DSP-11.
 XX KW Mouse; dual specificity phosphatase; DSP-11; Duchenne muscular dystrophy; KW MAP-kinase signalling cascade; cell proliferation; cancer; allergy; KW graft-versus-host disease; autoimmune disease; metabolic disease.
 XX OS Mus sp.
 XX PN WO200105983-A1.
 XX PD 25-JAN-2001.
 XX PF 19-JUL-2000; 2000WO-US19710.
 XX PR 20-JUL-1999; 99US-0144557.
 XX PA (CEPT-) CEPTYR INC.
 XX PI Luche RM, Wei B;
 XX DR WPI; 2001-147348/15.
 XX DR N-PSDB; AAF219563.

RESULT 8
 AAB73211
 ID AAB73211 standard; Protein; 150 AA.
 AC
 XX AAB73211;
 XX
 DE Murine phosphatase AA023073-
 DT 11-MAY-2001 (first entry)
 XX
 DE Murine dual specificity phosphatase DSP-11.
 XX KW Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia; KW cardiac dysfunction; vascular disorder; neuropathy; ectodermal dysplasia; congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease; KW Meobius syndrome; Bjornstad syndrome; Bannayan-Zonana syndrome; KW schizophrenia; hamartoma.
 XX OS Mus sp.
 XX PN WO200112819-A2.
 XX PD 22-FEB-2001.

PP Novel dual specificity phosphatase-11 dephosphorylating activated
PT mitogen-activated protein kinase, is used to identify agents inhibiting
PR the enzyme activity and modulate cell proliferation -
XX Example 3; Fig 6: 65pp; English.

Matches	21;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	91	VGVHCAALGFGFRGTMLACLYV	111						
Db	1	VGVHCAALGFGFRGTMLACLYV	21						

The present invention provides the protein and coding sequences of the human dual-specificity phosphatase **DSP-11**. The protein is involved in the MAP-kinase signalling cascade. The sequences can be used in the diagnosis and treatment of Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth and abnormal cell proliferation. The present sequence is the mouse **DSP-11** protein.

Search completed: November 4, 2002, 12:57:59
Job time: 33 sec

Query	Match	Best Local Similarity	Score	DB	Length
QY	TYDEANARGAEVGVHCAIGFGRGTMLACLYVER	100.0%	Pred. No. 9.6e-28	0	150
Dy	IYDEANARGAEVGVHCAIGFGRGTMLACLYVER	114	Mismatches 0;	Indels 0;	Gaps 0
Dy	IYDEANARGAEVGVHCAIGFGRGTMLACLYVER	114			

RESULT 10
AAB35273
ID AAB35273 standard; peptide; 21 AA.
XX
AC AAB35273;
XX
DT 08-MAY-2001 (first entry)
DE Human dual specificity phosphatase DSP-11 active site domain.
XX
KW Human; dual specificity phosphatase; DSP-11; Duchenne muscular dystrophy
KW MAP-kinase signalling cascade; cell proliferation; cancer; allergy;
KW graft-versus-host disease; autoimmune disease; metabolic disease.
XX
OS Homo sapiens.
XX
PN WO200105983-A1.
XX
PD 25-JAN-2001.
XX
PF 19-JUL-2000; 2000WO-US19710.
XX
PR 20-JUL-1999; 99US-0144557.
XX
PA (CEPT-) CEBTYR INC.
XX
PI Luche RM, Wei B;
XX
DR WPI; 2001-147308/15.
XX
PT Novel dual specificity phosphatase-11 dephosphorylating activated
PT mitogen-activated protein kinase, is used to identify agents inhibiting
PT the enzyme activity and modulate cell proliferation -
XX
PS Disclosure; Page 8; 65pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human dual-specificity phosphatase DSP-11. The protein is involved in the
CC MAP-kinase signalling cascade. The sequences can be used in the diagnosis
CC and treatment of Duchenne muscular dystrophy, cancer, graft-versus-host
CC disease, autoimmune diseases, allergies, metabolic diseases, abnormal
CC cell growth and abnormal cell proliferation. The present sequence is the
CC human DSP-11 active site domain.
XX
SQ Sequence 21 AA;

DEFINITION	UI-E-EJ0-ahu-1-09-0-01.s2 UI-E-EJ0 Homo sapiens cDNA clone
ACCESSION	BM676758
VERSION	BM676758.1
REFERENCE	GI:18986654
KEYWORDS	EST;
SOURCE	human.
ORGANISM	Homo sapiens
BASE COUNT	172 a 256 c 242 g 138 t
ORIGIN	(Stratagene) and superscript II RP (Life Technologies)*
Query Match	98.2%; Score 694.2; DB 12; Length 808;
Best Local Similarity	98.9%; Pred. No. 6.3e-99;
Matches	699; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY	1 TGACCGCGCTTCGCTTGCCCTTCCAGCGATGGCGCTCAGCCCCCAACTTCCTGG 60
Db	51 TGACCGCGCTTCGCTTGCCCTTCCAGCGATGGCGCTCAGCCCCCAACTTCCTGG 110
OY	61 GIGCTTCCGCGCCGCTGGGGAGATGGCGACTGGCGCTGGCGGGTCCCGCCACCTACAGTC 120
Db	111 GTGCCTCCGCGCCGCTGGGGAGATGGCGACTGGCGCTGGCGGGTCCCGCCACCTACAGTC 170
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OY	181 GACAGCTGCCCGGCTCACCTGCACCGSCTGGCGCATCCGACTTCGCCCGGCC 240
Db	231 GACAGCTGCCCGGCTCACCTGCACCGSCTGGCGCATCCGACTTCGCCCGGCC 290
OY	241 CCCACACAGACGACCGCTTGAGAGATGGGAGAGACGACGGAGAGCT 300
Db	291 CCCACACAGACGACCGCTTGAGAGATGGGAGAGACGACGGAGAGCT 350
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OY	421 GGCGCATGAGACGACTATGGCGAGAGAGCAGCTCGACCTACCGGAA 480
Db	471 AGCTCCATGGAGACTATGGCGAGAGAGCAGCTCGACCTACCGGAA 530
OY	481 TAAGGGCCTTAGGACCTCTAACCGGCTCACTCCCTTCCCATGTGTGATGG 540
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OY	541 GCGCAGAGATGAGGAACGAGCTAAGATAACCTCTAGCTCCATGGCTGAGA 600
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mRNA	linear
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 SOURCE Human.
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 740)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgb@rmail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at:
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 QY 601 CACTGAAGTGGCCACCCCTGCAAGCAGTGAAGGAGGAGCTGAC-TGCT 659
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 QY 660 TGTGAGATAATGAGTTAGAACCAAAAGAAAAA 698
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RESULT	7			Db	421	GGCTCATCGAGACCTATGACCAAGGAAGCAGCTTCCAGTCATCCAGCGAACGAA	480
LOCUS	BE263805	709 bp	mRNA linear EST 13-JUL-2000	Db	433	GGCTCCATCGAGACCTATGACCAAGGAAGCAGCTTCCAGTCATCCAGCGAACGAA	492
DEFINITION	601194169f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:5537904 5'			QY	481	TAAGGGCCTTAGTACCTCTACAGGCCCTACTCCCTCCATGCTGTCATGG	540
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REFERENCE	1 (bases 1 to 709) NIH-MGC http://mgc.ncbi.nih.gov/.			QY	601	CACTGAGTAGCCACCCCTCAGGGAGGCTCTGAATGAGGGAGGCTGTACTGCTT	660
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)			Db	613	CACTGAGTAGCCACCCCTCAGGGAGGCTCTGAATGAGGGAGGCTGTACTGCTT	671
TITLE	Unpublished (1999)			QY	661	GTGAAATAATGAGTTACGAACCaaaaaaa 698	
JOURNAL	Contact: Robert Strausberg, Ph.D.			Db	672	GTGAAATAATGAGTTACGAACCaaaaaaa 709	
COMMENT	Email: cgabps-r@email.nih.gov						
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QY	1	TGACCGCTCTCTGCCCCCTCCAGGATGCGCTCAGCCCCCACTCTCGG	60		ACCESSION	B1598433	
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Db	133	CGTGGGACCTGGGGCTGGCGACCTGGCTCCAGCGAGCGGGGG	192		AUTHORS	1 (bases 1 to 725) NIH-MC http://mgc.ncbi.nih.gov/.	
QY	181	GACAGCTGCCGCCCTCACCTGCACCCCTGCTGCTGCTGCTG	240		TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
Db	193	GACAGCTGCCGCCCTCACCTGCACCCCTGCTGCTGCTGCTG	252		JOURNAL	Unpublished (1999)	
QY	241	CCGACGAGATGCGACCGCTGGAGAGCTGGAGAGCTGGAGAG	300		COMMENT	Contact: Robert Strausberg, Ph.D.	
Db	253	CCGACGAGATGCGACCGCTGGAGAGCTGGAGAGCTGGAGAG	312			Email: cgabps-r@email.nih.gov	
QY	301	GTGGGAGTGCACCTGGCTGGCTGGCGACTGGCACCTCTGGCTG	360			Tissue Procurement: Miklos Palkovits, M.D., Ph.D.	
Db	313	GTGGGAGTGCACCTGGCTGGCTGGCGACTGGCACCTCTGGCTG	372			cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)	
BASE COUNT						cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
ORIGIN	145 a 233 c 216 g 131 t					DNA Sequencing by: Incyte Genomics, Inc.	

Query Match								
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QY 144 CACCCTCTGGCATCCGGACTCTGCCGGCCGGGGCCCCGACAGATGACGCTTG 264								
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QY 505 CAGGGCTACTCCCTCCAGTTGTCATGGTGAAGACACTGAGTAGCCACCCUTGAG 564								
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AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/								
JOURNAL Unpublished (1995)								
COMMENT Contact: Robert Strausberg, Ph.D. Email: cgabs-1@mail.nih.gov Tissue Procurement: DCID/DIP								
ORGANISM Homo sapiens								
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo; 1 (bases 1 to 944)								
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				REFERENCE 1 (bases 1 to 712)
				AUTHORS NIH/MGC http://mgc.ncbi.nlm.nih.gov/.
				TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
				JOURNAL Unpublished (1999)
				COMMENT Contact: Robert Strausberg, Ph.D. Email: cgbps-r@mail.nih.gov
				TISSUE Procurement: ARCC
				CDNA Library Preparation: Life Technologies, Inc.
				DNA Sequencing by: Incyte Genomics, Inc.
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				TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
				JOURNAL Unpublished (1999)
				COMMENT Contact: Robert Strausberg, Ph.D. Email: cgbps-r@mail.nih.gov
				TISSUE Procurement: ARCC
				CDNA Library Preparation: Ling Hong/Rubin Laboratory
				DNA Sequencing by: Incyte Genomics, Inc.
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				622 GGAGGCTCTGATGAGGGAGGTGTACTGCTTGTGACATATCTGAGSGRTT 681
				QY 685 CAAAAAMAAAAMAAAAAAAGAAA 707
				Db 682 CACGAAACACCGAACCAACACA 704

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QY	371	GCGGCTGGCTTCAGGAGATGCCATTGCGATTCGGAGAATCGCGAGATACGACCCGCTCCATCG	430	
DB	241	GCGGCTGGCTTCAGGAGATGCCATTGCGATTCGGAGAATCGCGAGATACGACCCGCTCCATCG	300	
QY	431	AGACCTATGAGGAGGAAAGCTCTCCAACTTACCGAGAACGAAATAGGGCT	490	
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REFERENCE	1 (bases 1 to 584)			
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/.			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: creapsr@mail.nih.gov			
Tissue	Procurement: Life Technologies, Inc.			
CDNA Library Preparation: Life Technologies, Inc.				
CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LNL)				
DNA Sequencing by: Invitrogen Inc.				
Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LNL at:				
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